

; CURRENT APPLICATION NUMBER: US/09/848,834A
 ; CURRENT FILING DATE: 2001-05-04
 ; PRIOR APPLICATION NUMBER: 60/202,328
 ; PRIOR FILING DATE: 2000-05-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 3
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 ; FEATURE:
 ; NAME/KEY: PEPTIDE
 ; LOCATION: (1)..(20)
 ; OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium
 ; OTHER INFORMATION: falciparum circumsporozoite (CSP) protein
 US-09-848-834A-3

Query Match 35.8%; Score 95; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 2.3e-05;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 17 DEKKIAKMEKASSVFNVNS 36
 DB 1 DEKKIAKMEKASSVFNVNS 20

RESULT 12
 US-10-239-313A-54
 ; Sequence 54, Application US/10239313A
 ; Publication No. US20030175285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KLINGUER - HAMOUR, Christine
 ; APPLICANT: CORVAIA, Nathalie
 ; APPLICANT: BECK, Alain
 ; APPLICANT: GOETSCH, Liliane
 ; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
 ; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
 ; TITLE OF INVENTION: OF A PHYSIOLOGICALLY ACCEPTABLE STRONG ACID
 ; FILE REFERENCE: 343 727 - US
 ; CURRENT APPLICATION NUMBER: US/10/239,313A
 ; CURRENT FILING DATE: 2002-09-19
 ; PRIOR APPLICATION NUMBER: FR 00/03711
 ; PRIOR FILING DATE: 2000-03-23
 ; PRIOR APPLICATION NUMBER: PCT 01/70772
 ; PRIOR FILING DATE: 2001-03-22
 ; NUMBER OF SEQ ID NOS: 697
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 54
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Plasmodium malariae
 US-10-239-313A-54

Query Match 33.6%; Score 89; DB 14; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.00013;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EKXIAKMEKASSVFNVNS 36
 DB 1 EKXIAKMEKASSVFNVNS 19

RESULT 13
 US-09-932-165-1482
 ; Sequence 1482, Application US/09932165
 ; Publication No. US20030134784A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RAITANO, ARTHUR
 ; APPLICANT: CHALLITA-EID, PIA M.
 ; APPLICANT: PARIS, MARY
 ; APPLICANT: SAFFRAN, DOUGLAS
 ; APPLICANT: AFAR, DANIEL
 ; APPLICANT: LEVIN, ELANA

; APPLICANT: HUBERT, RENE
 ; APPLICANT: GE, WANGMAO
 ; APPLICANT: JAKOBOVITZ, AYA
 ; TITLE OF INVENTION: NUCLEIC ACIDS AND CORRESPONDING PROTEINS ENTITLED
 ; TITLE OF INVENTION: 83P2H3 AND CatIF2B11 USEFUL IN TREATMENT AND
 ; TITLE OF INVENTION: DETECTION OF CANCER
 ; FILE REFERENCE: 51158-20014.00
 ; CURRENT APPLICATION NUMBER: US/09/932,165
 ; CURRENT FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: 60/226,329
 ; PRIOR FILING DATE: 2000-08-17
 ; NUMBER OF SEQ ID NOS: 1508
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1482
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-09-932-165-1482

Query Match 33.6%; Score 89; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EKXIAKMEKASSVFNVNS 36
 DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 14
 US-09-935-384-710
 ; Sequence 710, Application US/09935384
 ; Publication No. US2003016626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CHALLITA-EID, PIA
 ; APPLICANT: HUBERT, RENE
 ; APPLICANT: RAITANO, ARTHUR
 ; APPLICANT: AFAR, DANIEL
 ; APPLICANT: LEVIN, ELANA
 ; APPLICANT: PARIS, MARY
 ; APPLICANT: GE, WANGMAO
 ; APPLICANT: JAKOBOVITZ, AYA
 ; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1H4
 ; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
 ; TITLE OF INVENTION: OTHER CANCERS
 ; FILE REFERENCE: 51158-20033.00
 ; CURRENT APPLICATION NUMBER: US/09/935,384
 ; CURRENT FILING DATE: 2001-08-22
 ; PRIOR APPLICATION NUMBER: 60/227,098
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 783
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 710
 ; LENGTH: 21
 ; TYPE: PRT
 ; ORGANISM: Plasmodium falciparum
 US-09-935-384-710

Query Match 33.6%; Score 89; DB 10; Length 21;
 Best Local Similarity 100.0%; Pred. No. 0.00014;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 18 EKXIAKMEKASSVFNVNS 36
 DB 3 EKXIAKMEKASSVFNVNS 21

RESULT 15
 US-09-942-052-711
 ; Sequence 711, Application US/09942052
 ; Publication No. US20030170626A1
 ; GENERAL INFORMATION:
 ; APPLICANT: RAITANO, ARTHUR B.
 ; APPLICANT: PARIS, MARY

; APPLICANT: Hubert, Rene S.
; APPLICANT: Afar, Daniel
; APPLICANT: Ge, Wangmao
; APPLICANT: Challita-Eid, Pia M.
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 85P1B3
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 51158-20028.00
; CURRENT APPLICATION NUMBER: US/09/942,052
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 60/228,432
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 744
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 711
; LENGTH: 21
; TYPE: PRT
; ORGANISM: Plasmodium falciparum
US-09-942-052-711

Query Match 33.6%; Score 89; DB 10; Length 21;
Best Local Similarity 100.0%; Pred. No. 0.00014;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 EKXIAKMEKASSVFNVNS 36
| | | | | | | | | | | | | | | | | | | | | |
Db 3 EKXIAKMEKASSVFNVNS 21

Search completed: March 10, 2004, 10:25:50
Job time : 40.0856 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 15.8755 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-20
Perfect score: 265
Sequence: 1 XHWSVGLRPGSGPSLDEKK.....NVVNSSGSPSLHWSVGLRFX 51

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 78:**

1: P1r1:**

2: P1r2:**

3: P1r3:**

4: P1r4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	39.6	388	2 A39756	circumsporozoite p
2	99	37.4	405	2 S05428	circumsporozoite p
3	99	37.4	412	1 QZQAF	circumsporozoite p
4	93	37.4	424	2 A5433	circumsporozoite p
5	98	37.0	442	2 A54529	circumsporozoite p
6	66	24.9	332	1 QZQMB	circumsporozoite p
7	66	24.9	348	1 QZQBK	circumsporozoite p
8	63	23.8	264	2 A4969	circumsporozoite p
9	63	23.8	367	1 QZQMY	circumsporozoite p
10	62.5	23.6	82	2 I51365	gonadotropin-relea
11	60	22.6	98	2 I50739	gonadotropin-relea
12	59.5	22.5	315	2 F98295	hypothetical prote
13	59.5	22.5	1613	2 JE0272	low density lipopr
14	59.5	22.5	1613	2 JE0273	low density lipopr
15	59	22.3	429	2 A54504	circumsporozoite p
16	59	22.3	485	2 A60610	circumsporozoite p
17	58.5	22.1	74	2 I51092	gonadotropin relea
18	58.5	22.1	82	2 I51355	gonadotropin relea
19	58.5	22.1	82	2 I51331	gonadotropin relea
20	58.5	22.1	624	2 T38006	probable lysophosp
21	58	21.9	10	1 RHFG	gonadoliberin - sh
22	58	21.9	10	1 RHSG	gonadoliberin - sh
23	58	21.9	67	2 I78541	gonadoliberin prec
24	58	21.9	89	2 I51423	gonadoliberin prec
25	58	21.9	90	1 RHMS	gonadoliberin prec
26	58	21.9	92	1 RHUG	gonadoliberin prec
27	58	21.9	92	1 RHUG	gonadoliberin prec
28	58	21.9	345	2 T29416	hypothetical prote
29	58	21.9	464	2 C70122	thiophene and fura

gonadoliberin prec
hemocytin - silkwo
fdHE protein - Esc
affects formate de
affects formate de
conserved hypotet
interleukin-1beta
hypothetical prote
interleukin-1beta
interleukin-1beta
interleukin-1 beta
hypothetical prote
salmon-type gonado
hypothetical prote
probable lysophosp
36K antigen pra -

ALIGNMENTS

RESULT 1

A39756

circumsporozoite protein - Plasmodium reichenowi

C:Species: Plasmodium reichenowi

C>Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 20-Aug-1999

C:Accession: A39756

R:Fair, A.A.; Goldman, I.P.

J. Biol. Chem. 266, 6686-6689, 1991

A:Title: Circumsporozoite protein gene from Plasmodium reichenowi, a chimpanzee malaria

A:Reference number: A39756; MUID:91201303; PMID:2016283

A:Accession: A39756

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-388 <LAL>

A:Cross-references: GB:MS0972; NID:G160228; PIDN:AAA29561.1; PID:G160229

C:Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

F:312-366/Domain: thrombospondin type 1 repeat homology <THRI>

Query Match 39.6%; Score 105; DB 2; Length 388;

Best Local Similarity 58.5%; Pred. No. 6.7e-05;

Matches 24; Conservative 3; Mismatches 6; Indels 8; Gaps 1;

QY 7 LRPSSGSPSLD-----EKKTAKMEKASVFNVNSSSG 39

Db 337 IKPGSAGKPKDLDYNDLEKIKCKEKSSVFVNSSSG 377

RESULT 2

S05428

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate NF54)

C:Species: Plasmodium falciparum

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000

C:Accession: S05428; A45527; I60657

R:Campbell, J.R.

Nucleic Acids Res. 17, 5854, 1989

A:Title: DNA sequence of the gene encoding a Plasmodium falciparum malaria candidate va

A:Reference number: S05428; MUID:89345189; PMID:2668895

A:Accession: S05428

A:Status: translation not shown

A:Molecule type: DNA

A:Residues: 1-405 <CAM>

A:Cross-references: EMBL:X15363

R:Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.

Mol. Biochem. Parasitol. 35, 185-190, 1989

A:Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate u

A:Reference number: A45527; MUID:89364998; PMID:2671723

A:Accession: A45527

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-405 <CAS>

A:Cross-references: GB:M22982; GB:J04650; NID:G160168; PIDN:AAA29527.1; PID:G160169

R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.

```

Mol. Biochem. Parasitol. 37, 275-280, 1989
A>Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep
A;Reference number: A60657; MUID:90114334; PMID:2481827
A;Accession: I60657
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 319-336,354-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 37.4%; Score 99; DB 2; Length 405;
Best Local Similarity 56.1%; Pred. No. 0.00037; Indels 8; Gaps 1;
Matches 23; Conservative 3; Mismatches 7;

QY 7 LRPGSGPSLD-----EKKIAMEKASSVFNVNVSIG 39
DB 354 IKPGSANKPKDLDYNDIEKKICKMEKCSVFNVNVSIG 394
:||||:|||||
A;Molecule type: DNA
A;Residues: 1-412 <DAM>
A;Cross-references: GB:K02194; NID:G160160; PIDN:AAA29524.1; PID:G160161
A;Experimental source: clone 708
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;336-390/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 37.4%; Score 99; DB 1; Length 412;
Best Local Similarity 56.1%; Pred. No. 0.00038; Indels 8; Gaps 1;
Matches 23; Conservative 3; Mismatches 7;

QY 7 LRPGSGPSLD-----EKKIAMEKASSVFNVNVSIG 39
DB 361 IKPGSANKPKDLDYNDIEKKICKMEKCSVFNVNVSIG 401
:||||:|||||
A;Molecule type: DNA
A;Residues: 1-412 <DAM>
A;Cross-references: GB:K02194; NID:G160160; PIDN:AAA29524.1; PID:G160161
A;Experimental source: clone 708
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of the
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;336-390/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 37.4%; Score 99; DB 2; Length 424;
Best Local Similarity 56.1%; Pred. No. 0.00039; Indels 8; Gaps 1;
Matches 23; Conservative 3; Mismatches 7;

QY 7 LRPGSGPSLD-----EKKIAMEKASSVFNVNVSIG 39
DB 373 IKPGSANKPKDLDYNDIEKKICKMEKCSVFNVNVSIG 413
:||||:|||||
A;Molecule type: DNA
A;Residues: 1-424 <DEI>
A;Cross-references: GB:M19752; NID:G160216; PIDN:AAA29555.1; PID:G160217
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;348-402/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 37.4%; Score 99; DB 2; Length 424;
Best Local Similarity 56.1%; Pred. No. 0.00039; Indels 8; Gaps 1;
Matches 23; Conservative 3; Mismatches 7;

QY 7 LRPGSGPSLD-----EKKIAMEKASSVFNVNVSIG 39
DB 373 IKPGSANKPKDLDYNDIEKKICKMEKCSVFNVNVSIG 413
:||||:|||||
A;Molecule type: DNA
A;Residues: 1-424 <DEI>
A;Cross-references: GB:M19752; NID:G160216; PIDN:AAA29555.1; PID:G160217
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;348-402/Domain: thrombospondin type 1 repeat homology <THR1>

```

RESULT 5

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A54529
circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome)
C;Species: Plasmodium falciparum
C;Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000
C;Accession: A54529
R;Locker, M.J.; Schwarz, R.T.
Mol. Biochem. Parasitol. 22, 101-108, 1987
A>Title: Strain variation in the circumsporozoite protein gene of Plasmodium falciparum
A;Reference number: A54529; MUID:87115616; PMID:3543671
A;Accession: A54529
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-442 <LOC>
A;Cross-references: GB:M15505; NID:G160214; PIDN:AAA29554.1; PID:G160215
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>

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Query Match 37.0%; Score 98; DB 2; Length 442;
Best Local Similarity 56.1%; Pred. No. 0.00054; Indels 8; Gaps 1;
Matches 23; Conservative 3; Mismatches 7;

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QY 7 LRPGSGPSLD-----EKKIAMEKASSVFNVNVSIG 39
DB 391 IKPGSANKPKDLDYNDIEKKICKMEKCSVFNVNVSIG 431
:||||:|||||
A;Molecule type: DNA
A;Residues: 1-442 <LOC>
A;Cross-references: GB:M15505; NID:G160214; PIDN:AAA29554.1; PID:G160215
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
F;366-420/Domain: thrombospondin type 1 repeat homology <THR1>

```

RESULT 6

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OZQOMB
circumsporozoite protein precursor - Plasmodium berghei (strain NK65)
N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium berghei
C;Date: 30-Sep-1987 #sequence_revision 28-Jul-1995 #text_change 16-Jul-1999
C;Accession: A44948; A25083; S13446
R;Lanar, D.E.
Mol. Biochem. Parasitol. 39, 151-154, 1990
A>Title: Sequence of the circumsporozoite gene of Plasmodium berghei ANKA clone and NK6
A;Reference number: A44948; MUID:90158693; PMID:2406593
A;Accession: A44948
A;Molecule type: DNA
A;Residues: 1-332 <LAN>
A;Cross-references: GB:M28887
R;Eichinger, D.J.; Arnot, D.E.; Tam, J.P.; Nussenzweig, V.; Enea, V.
Mol. Cell. Biol. 6, 3965-3972, 1986
A>Title: Circumsporozoite protein of Plasmodium berghei: gene cloning and identification
A;Reference number: A25083; MUID:87089740; PMID:2432395
A;Accession: A25083
A;Molecule type: DNA
A;Residues: 1-26, 'I', 28-68, 'PMURR', 75-126, 'P', 128-134, 'PPNANDP', 135-332 <EIC>
A;Cross-references: GB:M14135; NID:G160245; PIDN:AAA29577.1; PID:G160246
R;Weber, J.L.; Egan, J.E.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.; Hockme
Exp. Parasitol. 63, 295-300, 1987
A>Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.
A;Reference number: S13446; MUID:87218962; PMID:3556207
A;Accession: S13446
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 61-122, 'A', 124-332 <WEB>
A;Cross-references: GB:M25445; NID:G160177; PIDN:AAA29531.1; PID:G160178
C;Comment: There are three distinct regions in the mature circumsporozoite protein, the
obc membrane-anchoring sequence.
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-332/Product: circumsporozoite protein #status predicted <MAT>
F;94-189/Region: 8-residue repeats
F;199-230/Region: 2-residue repeats
F;258-310/Domain: thrombospondin type 1 repeat homology <THR1>

```

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Query Match 24.9%; Score 66; DB 1; Length 332;

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A:Title: Three gonadotropin-releasing hormone genes in one organism suggest novel roles

A;Reference number: I50739; MUID:95396797; PMID:7667296
A;Accession: I50739
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-38 <WHI>
A;Cross-references: EMBL:U31865; NID:905398; PIDN:AAC59691.1; PID:905399
C;Superfamily: gonadoliberin

Query Match 22.6%; Score 60; DB 2; Length 98;
Best Local Similarity 30.4%; Pred. No. 3.7;
Matches 17; Conservative 6; Mismatches 23; Indels 10; Gaps 2;

QY 2 HWSYGLRPGSGPSLDE-----KKIAKMEKASSVFNVNSSGSPSLHWSYGL 48
DB 24 HWSYGLSPGK-RDLNFSDTLGNVVEFPVEAPCSVFGCAEESPPAKMTRVKNGL 78

RESULT 12
F98295
hypothetical protein AGR_L_2640gl [imported] - Agrobacterium tumefaciens (strain C58, C58)
C;Species: Agrobacterium tumefaciens
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C;Accession: F98295
R;Brown, S.D.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qureshi, B.; Goldman, R.; Goodner, B.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Liu, F.; Wollam, C.; Allinger, D.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743134
A;Accession: F98295
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-315 <KUR>
A;Cross-references: GB:AE007870; PIDN:AAK9888.1; PID:g15159835; GSPDB:GN00170
C;Genetics:
A;Gene: AGR_L_2640gl
A;Map position: linear chromosome

Query Match 22.5%; Score 59.5; DB 2; Length 315;
Best Local Similarity 34.5%; Pred. No. 16;
Matches 19; Conservative 4; Mismatches 13; Indels 19; Gaps 2;

QY 6 GLRPGSGPSLDEKKI-----AKMEKASSVFN--VNSSSGPS 41
DB 29 GCRQSGPLLEKEVKRKLFGALALVLAAPALAEATRGFATANNMMSGFS 83

RESULT 13
JE0272
low density lipoprotein receptor-related protein 6 - human
C;Species: Homo sapiens (man)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 08-Sep-2002
C;Accession: JE0272
R;Brown, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy, E.R.; Soderman, A.R.; Metzke, Biochem. Biophys. Res. Commun. 248, 879-888, 1998
A;Title: Isolation and characterization of LRP6, a novel member of the low density lipoprotein receptor family
A;Reference number: JE0272; MUID:98369644; PMID:9704021
A;Accession: JE0272
A;Molecule type: mRNA
A;Residues: 1-1613 <BRO>
A;Cross-references: GB:AF074264; NID:g3462526; PIDN:AAC33006.1; PID:g3462527
C;Genetics:
A;Gene: LRP6
A;Map position: 12p11-12p13
C;Superfamily: low density lipoprotein receptor-related protein; EGF homology; LDL receptor
F;286-323/Domain: EGF homology <EGF1>
F;592-627/Domain: EGF homology <EGF1>
F;1207-1243/Domain: EGF homology <EGF2>
F;1249-1285/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;1288-1322/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;1326-1360/Domain: LDL receptor ligand-binding repeat homology <LDL3>

Query Match 22.5%; Score 59.5; DB 2; Length 1613;
Best Local Similarity 26.4%; Pred. No. 1e+02;
Matches 19; Conservative 6; Mismatches 22; Indels 25; Gaps 0;

QY 4 SYGLRPGSGPSLDEKKIAKMEKASSVFN-----VVN-----SSS 38
DB 1448 SLISMGSGSPPYDRAHVTGASSSSSSSTKGTFFAILNPPSPATERSHYTMEFGYSN 1507

RESULT 14
JE0273
low density lipoprotein receptor-related protein 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 08-Sep-2002
C;Accession: JE0273
R;Brown, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy, E.R.; Soderman, A.R.; Metzke, Biochem. Biophys. Res. Commun. 248, 879-888, 1998
A;Title: Isolation and characterization of LRP6, a novel member of the low density lipoprotein receptor family
A;Reference number: JE0272; MUID:98369644; PMID:9704021
A;Accession: JE0273
A;Molecule type: mRNA
A;Residues: 1-1613 <BRO>
A;Cross-references: GB:AF074265; NID:g3462528; PIDN:AAC33007.1; PID:g3462529
C;Genetics:
A;Gene: LRP6
A;Map position: 6
C;Superfamily: low density lipoprotein receptor-related protein; EGF homology; LDL receptor
F;286-323/Domain: EGF homology <EGF1>
F;592-627/Domain: EGF homology <EGF1>
F;1207-1243/Domain: EGF homology <EGF2>
F;1249-1285/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;1288-1322/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;1326-1360/Domain: LDL receptor ligand-binding repeat homology <LDL3>

Query Match 22.5%; Score 59.5; DB 2; Length 1613;
Best Local Similarity 26.4%; Pred. No. 1e+02; 22; Indels 25; Gaps 2;

Matches 19; Conservative 6; Mismatches 22; Indels 25; Gaps 2;

QY 4 SYGLRPGSGPSLDEKKIAKMEKASSVFN-----VVN-----SSS 38
DB 1448 SLISMGSGSPPYDRAHVTGASSSSSSSTKGTFFAILNPPSPATERSHYTMEFGYSN 1507

QY 39 GPSLHWSYGLRP 50
DB 1508 SPSTHRSYSYRP 1519

RESULT 15
A54504
Circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)
C;Species: Plasmodium malariae
C;Date: 06-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
C;Accession: A54504
R;Lal, A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; McCutchan, Mol. Biochem. Parasitol. 30, 291-294, 1988
A;Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Reference number: A54504; MUID:89040027; PMID:3054537
A;Accession: A54504
A;Molecule type: DNA
A;Residues: 1-429 <LAL>
A;Cross-references: GB:J03992; NID:g160220; PIDN:AAA29557.1; PID:g160221
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
F;354-407/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 22.3%; Score 59; DB 2; Length 429;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 18 EKIAKMEKASSVFNVNSSSG 39

Matches 19; Conservative 6; Mismatches 22; Indels 25; Gaps 2;

QY 4 SYGLRPGSGPSLDEKKIAKMEKASSVFN-----VVN-----SSS 38
DB 1448 SLISMGSGSPPYDRAHVTGASSSSSSSTKGTFFAILNPPSPATERSHYTMEFGYSN 1507

QY 39 GPSLHWSYGLRP 50
DB 1508 SPSTHRSYSYRP 1519

RESULT 14
JE0273
low density lipoprotein receptor-related protein 6 - mouse
C;Species: Mus musculus (house mouse)
C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 08-Sep-2002
C;Accession: JE0273
R;Brown, S.D.; Twells, R.C.J.; Hey, P.J.; Cox, R.D.; Levy, E.R.; Soderman, A.R.; Metzke, Biochem. Biophys. Res. Commun. 248, 879-888, 1998
A;Title: Isolation and characterization of LRP6, a novel member of the low density lipoprotein receptor family
A;Reference number: JE0272; MUID:98369644; PMID:9704021
A;Accession: JE0273
A;Molecule type: mRNA
A;Residues: 1-1613 <BRO>
A;Cross-references: GB:AF074265; NID:g3462528; PIDN:AAC33007.1; PID:g3462529
C;Genetics:
A;Gene: LRP6
A;Map position: 6
C;Superfamily: low density lipoprotein receptor-related protein; EGF homology; LDL receptor
F;286-323/Domain: EGF homology <EGF1>
F;592-627/Domain: EGF homology <EGF1>
F;1207-1243/Domain: EGF homology <EGF2>
F;1249-1285/Domain: LDL receptor ligand-binding repeat homology <LDL1>
F;1288-1322/Domain: LDL receptor ligand-binding repeat homology <LDL>
F;1326-1360/Domain: LDL receptor ligand-binding repeat homology <LDL3>

Query Match 22.5%; Score 59.5; DB 2; Length 1613;
Best Local Similarity 26.4%; Pred. No. 1e+02; 22; Indels 25; Gaps 2;

Matches 19; Conservative 6; Mismatches 22; Indels 25; Gaps 2;

QY 4 SYGLRPGSGPSLDEKKIAKMEKASSVFN-----VVN-----SSS 38
DB 1448 SLISMGSGSPPYDRAHVTGASSSSSSSTKGTFFAILNPPSPATERSHYTMEFGYSN 1507

QY 39 GPSLHWSYGLRP 50
DB 1508 SPSTHRSYSYRP 1519

RESULT 15
A54504
Circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)
C;Species: Plasmodium malariae
C;Date: 06-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
C;Accession: A54504
R;Lal, A.A.; de la Cruz, V.F.; Campbell, G.H.; Procell, P.M.; Collins, W.E.; McCutchan, Mol. Biochem. Parasitol. 30, 291-294, 1988
A;Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Reference number: A54504; MUID:89040027; PMID:3054537
A;Accession: A54504
A;Molecule type: DNA
A;Residues: 1-429 <LAL>
A;Cross-references: GB:J03992; NID:g160220; PIDN:AAA29557.1; PID:g160221
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: tandem repeat
F;354-407/Domain: thrombospondin type 1 repeat homology <THR1>

Query Match 22.3%; Score 59; DB 2; Length 429;
Best Local Similarity 50.0%; Pred. No. 26;
Matches 11; Conservative 6; Mismatches 5; Indels 0; Gaps 0;

QY 18 EKIAKMEKASSVFNVNSSSG 39

Db 397 ETEICSLDKCSSIFNVVNSLG 418

Search completed: March 10, 2004, 09:16:53
Job time : 16.9343 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 17.8093 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-19

Perfect score: 244
Sequence: 1 XHWSYGLRPGSGPSLQYIK.....GITELSSGSLHWSYGLRXP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*
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4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*
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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114.5	46.9	47	1	US-08-446-692-35
2	114.5	46.9	47	2	US-08-488-851A-35
3	113.5	46.5	27	1	US-08-446-692-13
4	113.5	46.5	27	2	US-08-488-851A-13
5	108.5	44.5	699	2	US-08-694-865-16
6	108.5	44.5	699	3	US-09-124-491-16
7	108.5	44.5	699	4	US-09-383-912-16
8	106	43.4	49	1	US-08-387-156-4
9	106	43.4	49	2	US-08-694-865-4
10	106	43.4	49	2	US-08-878-748-4
11	106	43.4	49	3	US-09-124-491-4
12	106	43.4	49	4	US-09-383-912-4
13	106	43.4	544	1	US-08-387-156-10
14	106	43.4	544	2	US-08-694-865-10
15	106	43.4	544	2	US-08-878-748-10
16	106	43.4	544	3	US-09-124-491-10
17	106	43.4	544	4	US-09-383-912-10
18	106	43.4	977	1	US-08-387-156-8
19	106	43.4	977	2	US-08-694-865-8
20	106	43.4	977	2	US-08-878-748-8
21	106	43.4	977	3	US-09-124-491-8
22	106	43.4	977	4	US-09-383-912-8
23	91	37.3	40	4	US-09-026-276-35
24	91	37.3	40	4	US-09-964-201A-35
25	91	37.3	41	4	US-09-026-276-34
26	91	37.3	41	4	US-09-964-201A-34
27	90	36.9	44	1	US-07-690-983D-45

Sequence 6, Appli
Sequence 7, Appli
Sequence 47, Appli
Sequence 40, Appli
Sequence 26, Appli
Sequence 29, Appli
Sequence 30, Appli
Sequence 31, Appli
Sequence 26, Appli
Sequence 29, Appli
Sequence 30, Appli
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Sequence 43, Appli
Sequence 31, Appli
Sequence 31, Appli
Sequence 3, Appli
Sequence 16, Appli
Sequence 18, Appli

ALIGNMENTS

RESULT 1

US-08-446-692-35
; Sequence 35, Application US/08446692
; Patent No. 5759551

; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna

; APPLICANT: Wang, Chang Yi

; APPLICANT: Zamb, Timothy

; TITLE OF INVENTION: Immunogenic LHRH peptide constructs

; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines

; NUMBER OF SEQUENCES: 114

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Maria C.H. Lin

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: US

; ZIP: 10154-0053

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/446,692

; FILING DATE: 7-JUN-1995

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria C.H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4146 US2

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212)415-8745

; TELEFAX: (516)751-6849

; INFORMATION FOR SEQ ID NO: 35:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 47 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-08-446-692-35

Query Match 46.9%; Score 114.5; DB 1; Length 47;
Best Local Similarity 72.7%; Pred. No. 7.4e-08;
Matches 24; Conservative 6; Indels 3; Gaps 1;

Oy 13 GPSLOYIKANSKFIGITELSSGSLHWSYGLRXP 45

DB 17 GKKQYIKANSKFIGITELGGE--HWSYGLRP 46


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RESULT 2
US-08-488-351A-35
; Sequence 35, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; TYPE: amino acid
; LENGTH: 47 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-35
;
; Query Match 46.9%; Score 114.5; DB 2; Length 47;
; Best Local Similarity 72.7%; Pred. No. 7.4e-08;
; Matches 24; Conservative 6; Indels 3; Gaps 1;
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DB 17 GKKQYKSNKSPFGITELGGE---HWSYGLRP 45
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RESULT 3
US-08-446-692-13
; Sequence 13, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
```

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;
;
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-13
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; Query Match 46.5%; Score 113.5; DB 1; Length 27;
; Best Local Similarity 79.3%; Pred. No. 5.2e-08;
; Matches 23; Conservative 0; Mismatches 1; Indels 5; Gaps 1;
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QY 17 QYKANSKFIGITELSSGSPSLHWSYGLRP 45
DB 3 QYKANSKFIGITELE---HWSYGLRP 26
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RESULT 4
US-08-488-351A-13
; Sequence 13, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
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APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/383,912
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/694,865
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 699 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-383-912-16

Query Match 44.5%; Score 108.5; DB 4; Length 699;
Best Local Similarity 50.0%; Pred. No. 1e-05;
Matches 22; Conservative 0; Mismatches 11; Indels 11; Gaps 1;
QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSGPSLHWSYGLRP 45
Db 36 HWSYGLRPGSGQDSY-----GLRPGSGHWSYGLRP 68

RESULT 8
US-08-387-156-4
Sequence 4, Application US/08387156
Patent No. 5723129
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: REDMOND, MARK J.
APPLICANT: HUGHES, HUM P.A.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/387,156
FILING DATE: 10-FEB-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-387-156-4

Query Match 43.4%; Score 106; DB 1; Length 49;
Best Local Similarity 50.0%; Pred. No. 9.5e-07;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSGPSLHWSYGLRP 45
Db 2 HWSYGLRPGSGQDSY-----GLRPGSGHWSYGLRP 35

RESULT 9
US-08-694-865-4
Sequence 4, Application US/08694865
Patent No. 5837268
GENERAL INFORMATION:
APPLICANT: POTTER, ANDREW A.
APPLICANT: MANNS, JOHN G.
TITLE OF INVENTION: GRH-LEUKOTOXIN CHIMERAS
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: REED & ROBINS LLP
STREET: 285 HAMILTON AVENUE, SUITE 200
CITY: PALO ALTO
STATE: CA
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/694,865
FILING DATE: 09-AUG-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MCCracken, THOMAS P.
REGISTRATION NUMBER: 38,548
REFERENCE/DOCKET NUMBER: 9001-0016.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 49 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-694-865-4

Query Match 43.4%; Score 106; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 9.5e-07;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

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QY      2 HWSYGLRPGSGSPSLQYIKANSKFGITELSSGPSLHWSYGLRP 45
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Db      2 HWSYGLRPGSGSQDWSY-----GLR--PGSSQHWSYGLRP 35
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RESULT 10
US-08-878-748-4
; Sequence 4, Application US/08878748
; Patent No. 5969126
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUW P.A.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/878,748
; FILING DATE: 19-JUN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/387,156
; FILING DATE: 10-FEB-1995
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-878-748-4

Query Match          43.4%; Score 106; DB 2; Length 4
Best Local Similarity 50.0%; Pred. No. 9.5e-07;
Matches 22; Conservative 1; Mismatches 11; Indels

QY      2 HWSYGLRPGSGSPSLQYIKANSKFGITELSSGPSLHWSYGLRP 45
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Db      2 HWSYGLRPGSGSQDWSY-----GLR--PGSSQHWSYGLRP 35
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RESULT 11
US-09-124-491-4
; Sequence 4, Application US/09124491
; Patent No. 6022960
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANNS, JOHN G.
; TITLE OF INVENTION: GNRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34

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; APPLICATION NUMBER: US/09/383,912
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/694,865
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-912-4

Query Match 43.4%; Score 106; DB 4; Length 49;
Best Local Similarity 50.0%; Pred. No. 9.5e-07;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGSPSLHWSYGLRP 45
Db 2 HWSYGLRPGSGQDSY-----GLR--PGSSQHSYGLRP 35

RESULT 13
US-08-387-156-10
; Sequence 10, Application US/08387156
; Patent No. 5723129
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUW P.A.
; TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS
; STREET: 635 BRYANT STREET
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/387,156
; FILING DATE: 10-FEB-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,932
; FILING DATE: 14-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/779,171
; FILING DATE: 16-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: ROBINS, ROBERTA L.
; REGISTRATION NUMBER: 33,208
; REFERENCE/DOCKET NUMBER: 9001-0016.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 617-8999
; TELEFAX: (415) 327-3231
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid

; APPLICATION NUMBER: US/09/383,912
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/694,865
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-387-156-10

Query Match 43.4%; Score 106; DB 1; Length 544;
Best Local Similarity 50.0%; Pred. No. 1.6e-05;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGSPSLHWSYGLRP 45
Db 495 HWSYGLRPGSGQDSY-----GLR--PGSSQHSYGLRP 528

RESULT 14
US-08-694-865-10
; Sequence 10, Application US/08694865
; Patent No. 5837268
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: MANN, JOHN G.
; TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: REED & ROBINS LLP
; STREET: 285 HAMILTON AVENUE, SUITE 200
; CITY: PALO ALTO
; STATE: CA
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,865
; FILING DATE: 09-AUG-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, THOMAS P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0016.22
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)327-3400
; TELEFAX: (415)327-3231
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 544 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-694-865-10

Query Match 43.4%; Score 106; DB 2; Length 544;
Best Local Similarity 50.0%; Pred. No. 1.6e-05;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGSPSLHWSYGLRP 45
Db 495 HWSYGLRPGSGQDSY-----GLR--PGSSQHSYGLRP 528

RESULT 15
US-08-878-748-10
; Sequence 10, Application US/08878748
; Patent No. 5963126
; GENERAL INFORMATION:
; APPLICANT: POTTER, ANDREW A.
; APPLICANT: REDMOND, MARK J.
; APPLICANT: HUGHES, HUW P.A.
; TITLE OF INVENTION: GHRH-LEUKOTOXIN CHIMERAS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: REED & ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/878,748
FILING DATE: 19-JUN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/387,156
FILING DATE: 10-FEB-1995
APPLICATION NUMBER: US 07/960,932
FILING DATE: 14-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/779,171
FILING DATE: 16-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0016.21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 544 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-878-748-10

Query Match 43.4%; Score 106; DB 2; Length 544;
Best Local Similarity 50.0%; Pred. No. 1.6e-05;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

Qy 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGPSLHWSYGLRP 45
Db ||||| :
495 HWSYGLRPGSGQDWSY-----GLR--FGSSQHWSYGLRP 528

Search completed: March 10, 2004, 09:28:56
Job time : 17.8093 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 19.358 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-18
Perfect score: 274
Sequence: 1 XHWSYGLRPGSSGSLFNNF.....VSASHLEGPLHWSYGLRPX 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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2: /cgn2_6/ptodata/2/iaa/5B.COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A.COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B.COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS.COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	152	55.5	32	1	US-08-446-692-14
2	152	55.5	32	2	US-08-488-351A-14
3	120	43.8	188	4	US-09-396-937-14
4	114	41.6	31	5	PCT-US93-11703-64
5	114	41.6	173	4	US-09-396-937-20
6	114	41.6	452	1	US-07-618-312A-2
7	114	41.6	452	1	US-07-618-312A-4
8	114	41.6	452	1	US-08-110-786A-8
9	114	41.6	452	1	US-08-280-228-2
10	114	41.6	452	1	US-08-280-228-4
11	114	41.6	618	1	US-08-668-381A-5
12	114	41.6	853	4	US-08-913-880C-17
13	114	41.6	858	4	US-08-913-880C-16
14	114	41.6	860	4	US-08-913-880C-15
15	114	41.6	862	4	US-08-913-880C-14
16	114	41.6	865	4	US-08-913-880C-13
17	114	41.6	866	4	US-08-913-880C-12
18	114	41.6	874	4	US-08-913-880C-11
19	114	41.6	875	4	US-08-913-880C-10
20	114	41.6	1315	4	US-08-913-880C-1
21	112	40.9	21	1	US-07-610-525-1
22	112	40.9	21	2	US-08-661-052-12
23	112	40.9	21	2	US-08-460-502-8
24	112	40.9	21	2	US-08-724-774B-5
25	112	40.9	21	3	US-09-089-595-5
26	112	40.9	21	3	US-09-383-855-5
27	112	40.9	21	3	US-09-183-714B-5

Sequence 12, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 5, Appl
Sequence 12, Appl
Sequence 3, Appl
Sequence 8, Appl
Sequence 5, Appl
Sequence 3, Appl
Sequence 35, Appl
Sequence 2, Appl
Sequence 66, Appl
Sequence 5, Appl
Sequence 41, Appl
Sequence 8, Appl
Sequence 16, Appl
Sequence 16, Appl

28 112 40.9 21 3 US-09-188-082-12
29 112 40.9 21 3 US-09-171-969-10
30 112 40.9 21 4 US-09-364-088-12
31 112 40.9 21 4 US-09-642-281-5
32 112 40.9 21 4 US-09-102-716-12
33 112 40.9 21 4 US-08-432-483A-3
34 112 40.9 21 4 US-09-148-711A-8
35 112 40.9 21 4 US-09-589-717-5
36 112 40.9 21 4 US-08-945-289-3
37 112 40.9 21 4 US-09-396-937-35
38 112 40.9 21 4 US-09-405-986A-2
39 112 40.9 21 5 PCT-US93-11703-66
40 107 39.1 22 1 US-08-446-692-5
41 107 39.1 22 2 US-08-488-351A-5
42 107 39.1 22 3 US-09-100-409A-41
43 107 39.1 22 5 PCT-US95-13841-8
44 102.5 37.4 699 2 US-08-694-865-16
45 102.5 37.4 699 3 US-09-124-491-16

ALIGNMENTS

RESULT 1
US-08-446-692-14
; Sequence 14, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-14

Query Match 55.5%; Score 152; DB 1; Length 32;
Best Local Similarity 87.9%; Pred. No. 7.7e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 17 FNNFTVSFWMRLVKVSGASHLEGPLHWSYGLRP 49
Db 3 FNNFTVSFWMRLVKVSGASHLE----HWSYGLRP 31

RESULT 2
US-08-488-351A-14
; Sequence 14, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488.351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-14
Query Match 55.5%; Score 152; DB 2; Length 32;
Best Local Similarity 87.9%; Pred. No. 7.7e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 4; Gaps 1;
QY 17 FNNFTVFWLRVPKVSASHLEGSLHWSYGLRP 49
Db 3 FNNFTVFWLRVPKVSASHLE----HWSYGLRP 31
RESULT 3
US-09-396-937-14
; Sequence 14, Application US/09396937
; Patent No. 5645500
; GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S
; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper
; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand

; TITLE OF INVENTION: Activity
; FILE REFERENCE: 22021 PC 1
; CURRENT APPLICATION NUMBER: US/09/396,937
; CURRENT FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion of
; OTHER INFORMATION: murine OPG, residues 158-316 modified by
; OTHER INFORMATION: introduction of tetanus toxoid F30 epitope, and
; OTHER INFORMATION: His tag
US-09-396-937-14
Query Match 43.8%; Score 120; DB 4; Length 188;
Best Local Similarity 73.5%; Pred. No. 1.5e-08;
Matches 25; Conservative 2; Mismatches 3; Indels 4; Gaps 1;
QY 11 SSGPSLFNNFTVFWLRVPKVSASHLEGSLHWS 44
Db 107 SSHNLMFNNFTVFWLRVPKVSASHLE----NWS 136
RESULT 4
PCT-US93-11703-84
; Sequence 64, Application PC/TUS9311703
; GENERAL INFORMATION:
; APPLICANT: Chiron Mimotopes Pty. Ltd.
; TITLE OF INVENTION: T-Cell Epitopes
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Grant B. Green
; STREET: 4560 Horton St.
; CITY: Emeryville
; STATE: CA
; COUNTRY: USA
; ZIP: 94608
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/11703
; FILING DATE: 28-DEC-1993
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/984,852
; FILING DATE: 02-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, Grant D.
; REGISTRATION NUMBER: 31,259
; REFERENCE/DOCKET NUMBER: 0222.101
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-601-2706
; TELEFAX: 510-655-3542
; INFORMATION FOR SEQ ID NO: 64:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US93-11703-84
Query Match 41.6%; Score 114; DB 5; Length 31;
Best Local Similarity 95.5%; Pred. No. 1e-08;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 16 LFNNFTVFWLRVPKVSASHLE 37

Db :|||||
6 MFNFTVFWLRVPKVSASHLE 27

RESULT 5

US-09-396-937-20
; Sequence 20, Application US/09396937
; Patent No. 6645500

GENERAL INFORMATION:
; APPLICANT: M&E Biotech A/S

; APPLICANT: HALKIER, Torben
; APPLICANT: HAANING, Jesper

; TITLE OF INVENTION: Method for Down-Regulating Osteoprotegerin Ligand

; FILE REFERENCE: 20201 PC 1

; CURRENT APPLICATION NUMBER: US/09/396,937

; CURRENT FILING DATE: 1999-09-15

; NUMBER OF SEQ ID NOS: 35

; SEQ ID NO 20

; TYPE: PRT

; LENGTH: 173

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion between

; OTHER INFORMATION: murine OPGL, residues 158-316 with tetanus toxoid

; OTHER INFORMATION: P30 epitope introduced, and His tag

US-09-396-937-20

Query Match 41.6%; Score 114; DB 4; Length 173;

Best Local Similarity 54.5%; Pred. No. 9.6e-09; Indels 16; Gaps 1;
Matches 24; Conservative 2; Mismatches 2;

QY

17 FNNFTVFWLRVPKVSASHLE-----GPSLHWS 44

|||||

Db 78 FNNFTVFWLRVPKVSASHLEKTSIKIPSSHNLKMGSTKWS 121

RESULT 6

US-07-618-312A-2

; Sequence 2, Application US/07618312A
; Patent No. 5389540

GENERAL INFORMATION:

; APPLICANT: Makoff Dr, Andrew J

; APPLICANT: Romanos Dr, Michael A

; APPLICANT: Clare Dr, Jeffrey J

; APPLICANT: Fairweather Dr, Neil F

; TITLE OF INVENTION: VACCINES

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: 14th Floor

; STREET: 2200 Clarendon Boulevard,

; CITY: Arlington,

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/618,312A

FILING DATE: 19910516

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8926832.0

FILING DATE: 28-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9006097.1

FILING DATE: 17-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Crawford Mr, Arthur R

; REGISTRATION NUMBER: 25,327

; REFERENCE/DOCKET NUMBER: 510-51

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 0101 703 8750400

; TELEFAX: 0101 703 5253468

; TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-618-312A-2

Query Match 41.6%; Score 114; DB 1; Length 452;

Best Local Similarity 95.5%; Pred. No. 2.8e-07;

Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY

16 LFNNFTVFWLRVPKVSASHLE 37

|||||

Db 83 MFNFTVFWLRVPKVSASHLE 104

RESULT 7

US-07-618-312A-4

; Sequence 4, Application US/07618312A

; Patent No. 5389540

GENERAL INFORMATION:

; APPLICANT: Makoff Dr, Andrew J

; APPLICANT: Romanos Dr, Michael A

; APPLICANT: Clare Dr, Jeffrey J

; APPLICANT: Fairweather Dr, Neil F

; TITLE OF INVENTION: VACCINES

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: 14th Floor

; STREET: 2200 Clarendon Boulevard,

; CITY: Arlington,

; STATE: Virginia

; COUNTRY: U.S.A.

; ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/618,312A

FILING DATE: 19910516

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 8926832.0

FILING DATE: 28-NOV-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: GB 9006097.1

FILING DATE: 17-MAR-1990

ATTORNEY/AGENT INFORMATION:

NAME: Crawford Mr, Arthur R

REGISTRATION NUMBER: 25,327

REFERENCE/DOCKET NUMBER: 510-51

TELECOMMUNICATION INFORMATION:

TELEPHONE: 0101 703 8750400

TELEFAX: 0101 703 5253468

TELEX: 200797 NIXN UR

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 452 amino acids

; TYPE: AMINO ACID

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-07-618-312A-4

Query Match 41.6%; Score 114; DB 1; Length 452;

Best Local Similarity 95.5%; Pred. No. 2.8e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LFNNFTVSWLRVPKVSASHLE 37
Db 83 MFNNFTVSWLRVPKVSASHLE 104

RESULT 8

US-08-110-786A-8
; Sequence 8, Application US/08110786A
; Patent No. 5443966
; GENERAL INFORMATION:
; APPLICANT: FAIRWEATHER, Neil Fraser
; APPLICANT: MAKOFF, Andrew Joseph
; TITLE OF INVENTION: Expression of tetanus toxin fragment C
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nixon & Vanderhye P.C.
; STREET: 1100 No. 5443966th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/110,786A
; FILING DATE: 23-AUG-1993 1991
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/777,337
; FILING DATE: 29-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB90/00943
; FILING DATE: 20-JUN-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 8914122.0
; FILING DATE: 20 June 1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary J. Wilson
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-134
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-110-786A-8

Query Match 41.6%; Score 114; DB 1; Length 452;
Best Local Similarity 95.5%; Pred. No. 2.8e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LFNNFTVSWLRVPKVSASHLE 37
Db 83 MFNNFTVSWLRVPKVSASHLE 104

RESULT 9

US-08-280-228-2
; Sequence 2, Application US/08280228
; Patent No. 5571694
; GENERAL INFORMATION:
; APPLICANT: Makoff Dr, Andrew J

APPLICANT: Romanos Dr, Michael A

APPLICANT: Clare Dr, Jeffrey J

APPLICANT: Fairweather Dr, Neil F

TITLE OF INVENTION: VACCINES

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIXON & VANDERHYE P.C.

STREET: 1100 No. 5571694th Glebe Road

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

APPLICANT: Romanos Dr, Michael A
APPLICANT: Clare Dr, Jeffrey J
APPLICANT: Fairweather Dr, Neil F
TITLE OF INVENTION: VACCINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHYE P.C.
STREET: 1100 No. 5571694th Glebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/280,228
FILING DATE: 25-JUL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/618,312
FILING DATE: 27-NOV-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 8926832.0
FILING DATE: 28-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9006097.1
FILING DATE: 17-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mary J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 117-163
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
TELEX: 200797 NIXN UR
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 452 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-280-228-2

Query Match 41.6%; Score 114; DB 1; Length 452;
Best Local Similarity 95.5%; Pred. No. 2.8e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 16 LFNNFTVSWLRVPKVSASHLE 37
Db 83 MFNNFTVSWLRVPKVSASHLE 104

RESULT 10

US-08-280-228-4
; Sequence 4, Application US/08280228
; Patent No. 5571694
; GENERAL INFORMATION:
; APPLICANT: Makoff Dr, Andrew J
; APPLICANT: Romanos Dr, Michael A
; APPLICANT: Clare Dr, Jeffrey J
; APPLICANT: Fairweather Dr, Neil F
; TITLE OF INVENTION: VACCINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 5571694th Glebe Road
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.

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;
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/280,228
; FILING DATE: 25-JUL-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/618,312
; FILING DATE: 27-NOV-1990
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GS 8926532.0
; FILING DATE: 28-NOV-1989
; APPLICATION DATA:
; APPLICATION NUMBER: GB 9006097.1
; FILING DATE: 17-MAR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wilson, Mary J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 117-153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEFAX: (703) 816-4100
; TELEFAX: 200797 NIXN UR
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 452 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-280-228-4

Query Match 41.6%; Score 114; DB 1; Length 452;
Best Local Similarity 95.5%; Pred. No. 2.8e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 83 MFNNFTVSFWLRVPKVSASHLE 104

RESULT 11
US-08-668-381A-5
; Sequence 5, Application US/08668381A
; Patent No. 5780024
; GENERAL INFORMATION:
; APPLICANT: Brown, Robert H.
; APPLICANT: Fishman, Paul S.
; APPLICANT: Francis, Jonathan W.
; APPLICANT: Hosler, Betsy A.
; TITLE OF INVENTION: SUPEROXIDE DISMUTASE/TETANUS TOXIN
; TITLE OF INVENTION: FRAGMENT C HYBRID PROTEIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/668,381A
; FILING DATE: 21-JUN-1996
; CLASSIFICATION: 514
```

```
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/000,473
; FILING DATE: 23-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,164
; REFERENCE/DOCKET NUMBER: 00786/269001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEFAX: 200154
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 618 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-668-381A-5

Query Match 41.6%; Score 114; DB 1; Length 618;
Best Local Similarity 95.5%; Pred. No. 4.2e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 249 MFNNFTVSFWLRVPKVSASHLE 270

RESULT 12
US-08-913-880C-17
; Sequence 17, Application US/08913880C
; Patent No. 6372225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
; CURRENT FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 17
; LENGTH: 853
; TYPE: PRT
; ORGANISM: Clostridium tetani
; FEATURE:
; OTHER INFORMATION: Amino Acids 463 to 1315 of SEQ ID NO: 1
; US-08-913-880C-17

Query Match 41.6%; Score 114; DB 4; Length 853;
Best Local Similarity 95.5%; Pred. No. 6.2e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 484 MFNNFTVSFWLRVPKVSASHLE 505

RESULT 13
US-08-913-880C-16
; Sequence 16, Application US/08913880C
; Patent No. 6372225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; TITLE OF INVENTION: VACCINE
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
; CURRENT FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 16
; LENGTH: 858
; TYPE: PRT
; ORGANISM: Clostridium tetani
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; FEATURE:
; OTHER INFORMATION: Amino Acids 458 to 1315 of SEQ ID NO: 1
US-08-913-880C-16

Query Match      41.6%; Score 114; DB 4; Length 858;
Best Local Similarity 95.5%; Pred. No. 6.2e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 489 MFNNFTVSFWLRVPKVSASHLE 510

RESULT 14
US-08-913-880C-15
; Sequence 15, Application US/08913880C
; Patent No. 6372225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
; CURRENT FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 15
; LENGTH: 860
; TYPE: PRT
; ORGANISM: Clostridium tetani
; FEATURE:
; OTHER INFORMATION: Amino Acids 456 to 1315 of SEQ ID NO: 1
US-08-913-880C-15

Query Match      41.6%; Score 114; DB 4; Length 860;
Best Local Similarity 95.5%; Pred. No. 6.3e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 491 MFNNFTVSFWLRVPKVSASHLE 512

RESULT 15
US-08-913-880C-14
; Sequence 14, Application US/08913880C
; Patent No. 6372225
; GENERAL INFORMATION:
; APPLICANT: MATSUDA, Morihiro
; TITLE OF INVENTION: TETANUS TOXIN FUNCTIONAL FRAGMENT ANTIGEN AND TETANUS
; FILE REFERENCE: 216-380P
; CURRENT APPLICATION NUMBER: US/08/913,880C
; CURRENT FILING DATE: 1997-11-24
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Clostridium tetani
; FEATURE:
; OTHER INFORMATION: Amino Acids 454 to 1315 of SEQ ID NO: 1
US-08-913-880C-14

Query Match      41.6%; Score 114; DB 4; Length 862;
Best Local Similarity 95.5%; Pred. No. 6.3e-07;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 493 MFNNFTVSFWLRVPKVSASHLE 514

Search completed: March 10, 2004, 09:28:56
Job time : 19.358 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 14.3191 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-19

Perfect score: 244

Sequence: 1 XHWSYGLRPGSGPSLQYIK.....GITESSGSLHWSYGLRXP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	76	31.1	1315	1 BTCLTN	tentoxilysin (EC 3
2	69	28.3	82	2 I51365	gonadotropin-relea
3	65	26.6	74	2 I51092	gonadotropin relea
4	65	26.6	82	2 I51355	gonadotropin relea
5	65	26.6	82	2 I51331	gonadotropin relea
6	61	25.0	458	2 H87624	peptidase, M23/M37
7	60	24.6	447	2 B83563	conserved hypotet
8	59.5	24.4	66	2 S31029	gene 84 protein -
9	59.5	24.4	1172	2 T00065	hypothetical prote
10	59	24.2	123	2 C48677	ig heavy chain V-D
11	59	24.2	135	2 PH1494	ig heavy chain V r
12	58.5	24.0	90	1 RHMSG	gonadoliberin prec
13	58.5	24.0	374	2 E95361	probable mucronate
14	58	23.8	10	1 RHPGG	gonadoliberin - ph
15	58	23.8	10	1 RHSHG	gonadoliberin - ph
16	58	23.8	67	2 I78541	gonadoliberin prec
17	58	23.8	89	2 I51423	gonadoliberin prec
18	58	23.8	92	1 RHHUG	gonadoliberin prec
19	58	23.8	92	1 RHRTG	gonadoliberin prec
20	57	23.4	112	2 A27887	ig kappa chain V r
21	57	23.4	112	2 C27887	ig kappa chain V r
22	57	23.4	115	2 S38715	ig kappa chain V r
23	57	23.4	119	2 PH1518	ig heavy chain V r
24	57	23.4	119	2 PH1519	ig heavy chain V r
25	57	23.4	379	2 T44656	homoserine O-acety
26	57	23.0	530	2 F86467	hypothetical prote
27	56	23.0	102	2 PH1491	ig heavy chain V r
28	56	23.0	120	2 A49043	ig kappa chain V r
29	56	23.0	719	2 T52510	hypothetical prote

30 55 22.5 108 2 E32530
31 55 22.5 112 2 D27887
32 55 22.5 123 2 F48677
33 55 22.5 249 2 A41497
34 55 22.5 266 2 T30913
35 55 22.5 417 2 C82840
36 55 22.5 480 2 F82796
37 55 22.5 10 1 RHAQ1
38 54 22.1 92 2 I50644
39 54 22.1 98 2 B33936
40 54 22.1 100 2 S26334
41 54 22.1 103 2 PH1034
42 54 22.1 103 2 PH1030
43 54 22.1 103 2 PH1031
44 54 22.1 107 2 D32530
45 54 22.1 111 2 PL0257

ALIGNMENTS

RESULT 1

BTCLTN
tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
N/Alternate names: tetanus neurotoxin
C/Species: Clostridium tetani
C/Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 03-Jun-2002
C/Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
R/Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, M.
EMBO J. 5, 2495-2502, 1986
A/Title: Tetanus toxin: Primary structure, expression in E. coli, and homology with bot
A/Reference number: A25689; MUID:87053814; PMID:3536478
A/Accession: A25689
A/Molecule type: DNA
A/Residues: 1-1315 <EIS>
A/Cross-references: GS:X04436; NID:G40769; PIDN:CAA28033.1; PID:G40770
R/Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A/Title: The complete nucleotide sequence of tetanus toxin.
A/Reference number: A25757; MUID:87040747; PMID:3774547
A/Accession: A25757
A/Molecule type: DNA
A/Residues: 1-1315 <FAI>
A/Cross-references: GS:X06214; NID:G40773; PIDN:CAA29564.1; PID:G40774
A/Experimental source: strain CN3911
R/Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986
A/Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in
A/Reference number: A25194; MUID:86085672; PMID:3510187
A/Accession: A25194
A/Molecule type: DNA
A/Residues: 743-1315 <FA2>
A/Cross-references: GS:M12739; NID:G144920; PIDN:AAA23282.1; PID:G144921
A/Accession: B25194
A/Molecule type: protein
A/Residues: 865-894 <FA3>
R/Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsami, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A/Title: Isolation, purification, and characterization of fragment B, the NH-2-terminal
A/Reference number: A60759; MUID:90035436; PMID:2476476
A/Accession: A60759
A/Molecule type: protein
A/Residues: 461-475 <MAT>
R/Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989
A/Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A/Reference number: J500598; MUID:8903918; PMID:2463305
A/Contents: annotation; epitope region
R/Schiavo, G.; Benfenati, F.; Foulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.
Nature 359, 832-835, 1992
A/Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteoly
A/Reference number: S27125; MUID:93063293; PMID:1331807
A/Contents: annotation

```

RESULT 4
151355
gonadotropin releasing hormone - Atlantic salmon
151355
C/Species: Salmo salar (Atlantic salmon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 21-Jul-2000
C/Accession: I51356; I51355
R/Klungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.

```

A: Title: The Atlantic salmon prepro-gonadotropin releasing hormone gene and mRNA
A: Reference number: I51040; NCID: 92267241; PMID: 1587389
A: Accession: U53356
A: Status: Preliminary; translated from GB/EMBL/DBJ
A: Molecule type: mRNA
A: Cross-references: EMBL:X79709; NID: 9499341; PTD: 9499342

A:Molecule type: DNA
A:Residues: 1782 <K12>
A:Cross-references: EMBL:X74957; NID:G402786; PIDN:CAAS2912.1; PID:G402787
C:Genetics:
A:Gene: GnrH
A:Introns: 46/3; 73/3

Query Match	26.6%	Score 65;	DB 2;	Length 82;
Best Local Similarity	38.3%;	Pred. NO. 0.29;		
Matches 18:	Conservative	5;	Mismatches 20;	Indels 4;
Gaps	2;			

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Qy      2 HNSYGLRPGSSPSLYIKANSKFI--GITELSGGSLHWSYGLRP 45
        |||||
Db      25 HWSYGLMPGGK-RSVCELEATTKMDTGGVVALPEETSAHVSELRP 70
        |||||
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RESULT 5
151331

C:Species: *Salvelinus fontinalis* (brook trout)
C:Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 05-Nov-1999
C:Accession: E51331
R:Klungland, H.; Lorens, J.B.; Andersen, O.; Kisen, G.O.; Alestrom, P.
Mol. Cell. Endocrinol. 84, 167-174, 1992
A:Title: The Atlantic salmon prepro-gonadotropin releasing hormone gene and mRNA
A:Reference number: 151040; PMID:92267241; PMID:1587389

A: Molecule type: DNA
 A: Residues: 1-82 <KIU>
 A: Cross-references: EMBL:X79712; NID:G499336; PIDN:CAA56151.1; PID:G499337
 C: Genetics:
 A: Gene: GNRH
 A: Introns: 46/3; 73/3
 26.6%; Score 65; DB 2; Length 82;
 Query Match Best Local Similarity 38.3%; Pred. No. 0.29;
 Matches 18: Conservative 5; Mismatches 20; Indels 4; Gaps 2;

QY 2 HWSYGLRPGSSGPSLQYIKANSKFI --GITELSSGPSLHWSYGLRP 45

[illegible]

C:\Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 30-Sep-2000

C:\Accession: E95361

C:\Authors: R.F.; Fisher, T.; Jones, T.; Komp, C.; Abola, A.P.; Barloy-Hub...

C:\Title: Nucleotide sequence and predicted functions of the entire Sinorhizobium

C:\Reference number: A95262; MUID:21396509; PMID:11481432

C:\Accession: E95361

C:\Status: preliminary

C:\Molecule type: DNA

C:\Residues: 1-374 <R>

C:\Cross-references: GB:AF006469; PIDN:AAK65455.1; PID:gl4523923; GSPDB:GN000

C:\Experimental source: strain 1021, megaplasmid pSymA

C:\Authors: F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; B;

C:\Title: The composite genome of the legume symbiont Sinorhizobium meliloti

C:\Reference number: A96039; MUID:21368234; PMID:11474104

C:\Contents: annotation

C:\Genetics:

C:\Gene: Sma1461

C:\Genome: plasmid

C:\Keywords: intramolecular lyase; isomerase

Query Match 24.0%; Score 58.5; DB 2; Length 374;

Best Local Similarity 41.2%; Pred.No.11;

Matches 14; Conservative 6; Mismatches 13; Indels 1; Gaps

QY 2 HWSYGLRGSGSPSLQVYKANSKFIGITELSSGP 35

DB 21 HWSYGIIR-SPAVNLIEADDTGVIGECTVAP 53

RESULT 14

RHPGG

gonadolibirin - pig

C:\Species: Sus scrofa domestica (domestic pig)

C:\Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 18-Mar-1997

C:\Accession: A01411

C:\Residues: 1-10 <BAB>

C:\Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid

C:\Reference number: A90176; MUID:72117544; PMID:4946057

C:\Accession: A01411

C:\Molecule type: protein

C:\Residues: 1-10 <BAB>

C:\Title: Synthesis of the porcine LH- and FSH-releasing hormone by the solid

C:\Reference number: A90176; MUID:72065376; PMID:4942726

C:\Contents: annotation; synthesis

C:\Note: the synthetic and natural hormones have the same physicochemical

C:\Residues: 1-10 <BAB>

C:\Title: Synthesis of the porcine LH- and FSH-releasing hormone

C:\Reference number: A90175; MUID:72117544; PMID:4946275

C:\Contents: annotation

C:\Note: Trp-3 appears to be essential for biological activity

C:\Comment: This hypothalamic hormone stimulates the secretion of both luteal

C:\Superfamily: gonadolibirin

C:\Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid

F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F1/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.8%; Score 58; DB 1; Length 10;

Best Local Similarity 100.0%; Pred.No.0.2;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps

probable muconate cycloisomerase (EC 5.5.1.1) [imported] - Sinorhizobium meliloti (strain E95361)
C:Species: Sinorhizobium meliloti

Db 2 HWSYGLRPG 10

RESULT 15

RHSHG

gonadoliberin - sheep
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 18-Mar-1997
 C:Accession: A93780; A01411
 R:Burgus, R.; Butcher, M.; Amoss, M.; Ling, N.; Monahan, M.; Rivier, J.; Fellows, R.; Bl
 Proc. Natl. Acad. Sci. U.S.A. 69, 278-282, 1972
 A:Title: Primary structure of the ovine hypothalamic luteinizing hormone-releasing facto
 A:Reference number: A93780; MUID:72094314; PMID:4550508
 A:Accession: A93780
 A:Molecule type: protein
 A:Residues: 1-10 <BUR>
 A:Note: the natural and synthetic hormones have the same biological activity
 C:Comment: This hypothalamic hormone stimulates the secretion of both luteinizing and fo
 C:Superfamily: gonadoliberin
 C:Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
 F:1/Modified site: pyroglutamic acid (Gln) #status experimental
 F:10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 23.8%; Score 58; DB 1; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.2; Mismatches 0; Indels 0; Gaps 0;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPG 10

|||||||

Db 2 HWSYGLRPG 10

Search completed: March 10, 2004, 09:16:52
 Job time : 14.3779 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:53 ; Search time 8.41245 Seconds
(without alignments)
284.724 Million cell updates/sec

Title: US-09-848-834A-19

Perfect score: 244

Sequence: 1 XHWSYGLRPGSGPSLQYIK.....GITELSSGSPSLHWSYGLRXP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	31.1	1314	1	TETX_CLOTE
2	69	28.3	82	1	GON3_SALTR
3	65	26.6	74	1	GON3_ONCTS
4	65	26.6	82	1	GON3_SALSA
5	64	26.2	74	1	GON3_ONCWY
6	62.5	25.6	63	1	GON1_MESAU
7	60	24.6	61	1	GON1_SHEEP
8	59.5	24.4	66	1	VGB4_EPMU5
9	59.5	24.4	90	1	GON1_RANCA
10	59.5	24.4	1259	1	AUT2_HUMAN
11	58.5	24.0	90	1	GON1_MOUSE
12	58	23.8	67	1	GON1_MACMU
13	58	23.8	89	1	GON1_XENLA
14	58	23.8	91	1	GON1_PIG
15	58	23.8	92	1	GON1_HUMAN
16	58	23.8	92	1	GON1_RAT
17	58	23.8	92	1	GON1_TUPGB
18	57	23.4	90	1	GON3_DICLA
19	57	23.4	99	1	GON1_DICLA
20	57	23.4	379	1	MTX1_LEPME
21	55	22.5	249	1	PRR_MYCLE
22	55	22.5	266	1	XINC_CALSA
23	55	22.5	480	1	Y523_XYLFA
24	54	22.1	10	1	GON1_ALLMI
25	54	22.1	92	1	GON1_CHICK
26	53.5	21.9	148	1	HIL_MYTCA
27	53.5	21.9	202	1	HIL_MYTCA
28	53.5	21.9	596	1	SDP_EIMBO
29	53.5	21.9	733	1	VINE_MOUSE
30	53.5	21.9	940	1	MA24_SCHCO
31	53	21.7	299	1	YXCC_CYAPA
32	53	21.7	485	1	RT16_MYXAX
33	53	21.7	539	1	RN37_MOUSE

34 53 21.7 575 1 ACEA_LYCES
35 52.5 21.5 1191 1 LM22_MOUSE
36 52 21.3 82 1 GON3_ONCWA
37 52 21.3 89 1 GON3_PORNO
38 52 21.3 90 1 GON3_PAGNA
39 52 21.3 90 1 GON3_SPAU
40 52 21.3 94 1 GON1_HAPBU
41 52 21.3 95 1 GON1_MORSA
42 52 21.3 95 1 GON1_PAGMA
43 52 21.3 95 1 GON1_SPAU
44 51.5 21.1 366 1 METX_LEPIN
45 51.5 21.1 493 1 C6AD_DROME

ALIGNMENTS

RESULT 1
TETX_CLOTE
ID TETX_CLOTE STANDARD; PRT; 1314 AA.
AC P04958;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DE Tetanus toxin precursor (EC 3.4.24.68) (Tetoxylisin) [Contains:
DE Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
DE chain (Tetanus toxin chain H)].
GN TETX OR CTP60.
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=87053814; PubMed=3536478;
RA Biesel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
RA Weller U., Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and
RT homology with botulinum toxins.";
RL EMBO J. 5:2495-2502(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CN3911; PLASMID=75 Kbp;
RX MEDLINE=87040747; PubMed=3774547;
RA Fairweather N.F., Lyness V.A.;
RT "The complete nucleotide sequence of tetanus toxin.";
RL Nucleic Acids Res. 14:7809-7812(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / F88; PLASMID=PB88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baumer S., Fricke W.F., Wierse A., Liesegang H.,
RA Decker I., Herzberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
RN [4]
RP SEQUENCE OF 742-1314 FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=86085672; PubMed=3510187;
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
RT fragment C in Escherichia coli.";
RL J. Bacteriol. 165:21-27(1986).
RN [5]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=90201034; PubMed=2108021;
RA Kriegstein K., Henschen A., Weller U., Habermann E.;
RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
RT in tetanus toxin.";

P49297 lycopersico
Q61092 mus musculus
P30973 oncorhynchu
P51922 porichthys
P51921 pagrus major
P51923 sparus major
P51918 haplochromi
O73812 morone saxa
P70074 pagrus major
P51919 sparus major
Q85410 leptospira
Q94409 drosophila

RL Eur. J. Biochem. 188:39-45(1990).
 RN [6].
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Kriegstein K.G., Henschen A.H., Weller U., Habermann E.;
 RT "Limited proteolysis of tetanus toxin. Relation to activity and
 RL identification of cleavage sites";
 RN Eur. J. Biochem. 202:41-51(1991).
 RP [7].
 RX IDENTIFICATION AS ZINC-PROTEASE.
 RA MEDLINE=93010348; PubMed=1396558;
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "Tetanus toxin is a zinc protein and its inhibition of
 RT neurotransmitter release and protease activity depend on zinc";
 RL EMBO J. 11:3577-3583(1992).
 RN [8].
 RP IDENTIFICATION OF SUBSTRATE.
 RX MEDLINE=93063293; PubMed=1331807;
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Dasgupta B.R., Montecucco C.;
 RT "Tetanus and botulinum-B neurotoxins block neurotransmitter release
 RT by proteolytic cleavage of synaptobrevin";
 RL Nature 359:832-835(1992).
 RN [9].
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RX MEDLINE=97475217; PubMed=9334741;
 RA Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 RT neurotoxin";
 RL Nat. Struct. Biol. 4:788-792(1997).
 CC -!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 CC BOND OF SYNAPTOSOMAL-2.
 CC -!- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
 CC synaptobrevin 2.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 CC YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 CC AND ARE NON-TOXIC AFTER SEPARATION.
 CC -!- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 CC GANGLIOSIDE RECEPTORS.
 CC -!- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 DR EMBL; X04436; CAA28033.1; -.
 DR EMBL; X06214; CAA29564.1; -.
 DR EMBL; AF528097; AAO37454.1; -.
 DR EMBL; M12739; AAA23282.1; -.
 DR PIR; A25689; BTCLTN.
 DR PDB; 1AF9; 29-APR-98.
 DR PDB; 1ABD; 14-OCT-98.
 DR PDB; 1DOH; 27-MAR-00.
 DR PDB; 1DFQ; 24-MAR-00.
 DR PDB; 1DIW; 24-MAR-00.
 DR PDB; 1DLL; 24-MAR-00.
 DR PDB; 1PV3; 05-SEP-01.
 DR MEROPS; M27_001; -.
 DR InterPro; IPR008985; ConsA like lec_gl.
 DR InterPro; IPR002160; Kunitz legume.
 DR InterPro; IPR006025; Pept_M_Zn_BS.

DR InterPro; IPR000395; Peptidase_M27.
 DR Pfam; PF01742; Peptidase_M27; 1.
 DR PRINTS; PRO0760; BONTOXILYSIN.
 DR PRODOM; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 FT 3D-structure; Complete proteome.
 FT INIT_MET 0
 FT CHAIN 1 456 TETANUS TOXIN LIGHT CHAIN.
 FT CHAIN 457 1314 TETANUS TOXIN HEAVY CHAIN.
 FT METAL 232 232 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT_SITE 233 233 BY SIMILARITY.
 FT METAL 236 236 ZINC (CATALYTIC) (BY SIMILARITY).
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 669 689 POTENTIAL.
 FT DISULFID 438 466 INTERCHAIN.
 FT DISULFID 1076 1092
 FT HELIX 876 882
 FT TURN 883 883
 FT TURN 884 891
 FT STRAND 892 893
 FT TURN 894 897
 FT STRAND 904 907
 FT TURN 909 910
 FT STRAND 912 915
 FT STRAND 920 925
 FT TURN 928 929
 FT STRAND 932 935
 FT STRAND 938 940
 FT TURN 941 946
 FT STRAND 949 956
 FT HELIX 962 968
 FT TURN 969 970
 FT STRAND 972 977
 FT STRAND 980 981
 FT HELIX 983 985
 FT STRAND 987 995
 FT TURN 996 997
 FT STRAND 998 1004
 FT TURN 1006 1007
 FT STRAND 1010 1016
 FT STRAND 1020 1020
 FT TURN 1021 1022
 FT STRAND 1031 1037
 FT TURN 1039 1040
 FT STRAND 1042 1047
 FT TURN 1048 1049
 FT STRAND 1050 1056
 FT TURN 1058 1059
 FT STRAND 1068 1074
 FT TURN 1079 1080
 FT STRAND 1082 1091
 FT HELIX 1097 1105
 FT TURN 1106 1107
 FT STRAND 1112 1112
 FT STRAND 1114 1114
 FT TURN 1116 1117
 FT STRAND 1120 1120
 FT STRAND 1122 1122
 FT TURN 1123 1124
 FT STRAND 1127 1131
 FT HELIX 1132 1134
 FT TURN 1135 1136
 FT STRAND 1137 1141
 FT TURN 1144 1145
 FT STRAND 1148 1152
 FT TURN 1155 1158
 FT STRAND 1159 1162
 FT TURN 1163 1166
 FT STRAND 1173 1178
 FT TURN 1184 1185
 FT STRAND 1188 1188
 FT STRAND 1190 1190

OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_taxid=8030, 8038, 8023;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.salar, and S.fontinalis; TISSUE=Hypothalamus;
RX MEDLINE=92267241; PubMed=1587389;
RA Klungland H., Lorens J.B., Andersen O., Kisen G.O., Alestroem P.;
RT "The Atlantic salmon prepro-gonadotropin releasing hormone gene and
mRNA".
RL Mol. Cell. Endocrinol. 84:167-174(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=O.nerka; TISSUE=Liver;
RX MEDLINE=96227617; PubMed=8674859;
RA Coe I.R., von Schalburg K.R., Sherwood N.M.;
RT "Characterization of the Pacific salmon gonadotropin-releasing hormone
gene, copy number and transcription start site".
RL Mol. Cell. Endocrinol. 115:113-122(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=O.nerka; STRAIN=Nikko; TISSUE=Brain;
RX MEDLINE=96020547; PubMed=8546809;
RA Ashihara M., Suzuki M., Kubokawa K., Aida K., Urano A.;
RT "Two differing precursor genes for the salmon-type gonadotropin-
releasing hormone exist in salmonids".
RL J. Mol. Endocrinol. 15:1-9(1995).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Brain.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC
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CC
DR EMBL; X79709; CAA56348.1; -
DR EMBL; X74957; CAA52912.1; -
DR EMBL; X79712; CAA56151.1; -
DR EMBL; X91408; CAA62751.1; -
DR EMBL; D31869; BAA06667.1; -
DR PIR; I51331; I51331.
DR PIR; I51356; I51355.
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 82 PROGNADOLIBERIN III.
FT PEPTIDE 24 33 GONADOLIBERIN III.
FT PEPTIDE 37 82 GnRH-ASSOCIATED PEPTIDE III.
FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID
FT MOD_RES 33 33 (BY SIMILARITY).
FT MOD_RES 81 81 AMIDATION (G-34 PROVIDE AMIDE GROUP).
FT VARIANT 81 81 H -> Q.
FT SEQUENCE 82 AA; 9143 MW; 8053F4E44A765408 CRC64;
Query Match 26.6%; Score 65; DB 1; Length 82;
Best Local Similarity 38.3%; Pred. No. 0.084; Mismatches 5; Indels 4; Gaps 2;
Matches 18; Conservative 5;
QY 2 HWSYGLRPGSGPSLQYIKANSKFI---GITESSGPSLHWSYGLRP 45
DB 25 HWSYGLWPGK-RSVGELEATIKMDTGCVVALPEETSAHVSRLRP 70
RESULT 5
GON3_ONCMY STANDARD; PRT; 74 AA.
ID -GON3_ONCMY

AC P55246;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gonadoliberin III precursor (Gonadotropin-releasing hormone III)
DE (GnRH-III) (LH-RH III) (Luliberin III) (Fragment).
GN GNH3.
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_taxid=8022;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Klungland H., Anderson O., Alestroem P.;
RT "The salmon gonadotropin-releasing hormone encoding gene in
salmonids".
RL Mol. Mar. Biol. Biotechnol. 1:420-425(1992).
RN [2]
RP SEQUENCE OF 1-65 FROM N.A.
RX MEDLINE=93386322; PubMed=1308825;
RA Alestroem P., Kisen G., Klungland H., Andersen O.;
RT "Fish gonadotropin-releasing hormone gene and molecular approaches
for control of sexual maturation: development of a transgenic fish
model".
RL Mol. Mar. Biol. Biotechnol. 1:376-379(1992).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the GnRH family.
CC
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CC
DR EMBL; X79710; CAA56149.1; -
DR EMBL; S65569; AAD13966.1; -
DR InterPro; IPR002012; GnRH.
DR Pfam; PF00446; GnRH; 1.
DR PROSITE; PS00473; GnRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
KW Signal; Pyrrolidone carboxylic acid.
FT NON_TER 1 15 BY SIMILARITY.
FT SIGNAL 16 74 PROGNADOLIBERIN III.
FT CHAIN 16 74 GONADOLIBERIN III.
FT PEPTIDE 16 25 GnRH-ASSOCIATED PEPTIDE III.
FT PEPTIDE 29 74 PYRROLIDONE CARBOXYLIC ACID
FT MOD_RES 16 16 (BY SIMILARITY).
FT MOD_RES 25 25 AMIDATION (G-26 PROVIDE AMIDE GROUP).
FT SEQUENCE 74 AA; 8254 MW; BD63C46D8228EP84 CRC64;
Query Match 26.2%; Score 64; DB 1; Length 74;
Best Local Similarity 38.3%; Pred. No. 0.1; Mismatches 5; Indels 4; Gaps 2;
Matches 18; Conservative 5;
QY 2 HWSYGLRPGSGPSLQYIKANSKFI---GITESSGPSLHWSYGLRP 45
DB 17 HWSYGLWPGK-RSVGELEATIKMDTGCVVLPETSAHVSRLRP 62
RESULT 6
GON1_MESAU STANDARD; PRT; 63 AA.
ID -GON1_MESAU
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)]


```
RX MEDLINE=93211282; PubMed=8459766;
RA Hatfull G.F., Sarkis G.J.;
RT "DNA sequence, structure and gene expression of mycobacteriophage L5;
RL a phase system for mycobacterial genetics.";
RL Mol. Microbiol. 7:395-405(1993).
CC -----
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CC -----
CC EMBL; Z18946; CRA79460.1; -
DR PIR; S31029; S31029.
SQ SEQUENCE 66 AA; 7424 MW; 9C7104C7A4FA74A5 CRC64;
Query Match 24.4%; Score 59.5; DB 1; Length 66;
Best Local Similarity 45.5%; Pred. No. 0.35;
Matches 15; Conservative 2; Mismatches 7; Indels 9; Gaps 2;
QY 5 YGL-----RPGSSGSLQYIKANSKFIGITELS 32
DB 36 YGFEVDVYEPGESG-----YIKRNGKFGVTWEVS 64
RESULT 9
GONI_RANCA
ID GONI_RANCA STANDARD; PRT; 90 AA.
AC Q90Y63;
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Progonadolibirin I precursor (Contains: Gonadolibirin I (LHRH I)
DE (Luteinizing hormone releasing hormone I) (Gonadotropin releasing
DE hormone I) (GNRH I) (Luliberin I); GNRH-associated peptide I (GAP1)].
GN GNRH1 OR GNRH.
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8400;
RN [1]
SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC TISSUE=Forebrain;
RX MEDLINE=21102951; PubMed=11170016;
RA Wang L., Yoo M.S., Kang H.M., Im W.B., Choi H.S., Bogerd J.,
RA Kwon H.B.;
RT "Cloning and characterization of cDNAs encoding the GNRH1 and GNRH2
RT precursors from bullfrog (Rana catesbeiana).";
RL J. Exp. Zool. 289:190-201(2001).
CC -!- FUNCTION: Stimulates the secretion of gonadotropins (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Forebrain.
CC -!- DEVELOPMENTAL STAGE: Expressed at significantly higher levels
CC during post-breedings. Not expressed in pituitary.
CC -!- SIMILARITY: Belongs to the GNRH family.
CC -----
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CC -----
CC EMBL; AF188754; AAL05972.1; -
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0005183; F:Luteinizing hormone-releasing factor activity; NAS.
DR GO; GO:0009755; P:hormone mediated signaling; NAS.
DR GO; GO:0000003; P:reproduction; NAS.
DR InterPro; IPR002012; GNRH.
```

```
DR InterPro; IPR004079; Gonadolibirin1.
DR Pfam; PF00446; GNRH; 1.
DR PRINTS; PRO1541; GONADOLIBRN1.
DR PROSITE; PS00473; GNRH; 1.
KW Cleavage on pair of basic residues; Hormone; Amidation; Signal;
KW Pyroglutamate carboxylic acid.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 90 PROGNADOLIBIRIN I.
FT PEPTIDE 25 34 GONADOLIBIRIN I.
FT PEPTIDE 38 86 GNRH-ASSOCIATED PEPTIDE I (BY
FT SIMILARITY).
FT MOD_RES 25 25 PYRROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT MOD_RES 34 34 AMIDATION (G-35 PROVIDE AMIDE GROUP) (BY
FT SIMILARITY).
SQ SEQUENCE 90 AA; 10291 MW; 317203B4E3DA2FE7 CRC64;
Query Match 24.4%; Score 59.5; DB 1; Length 90;
Best Local Similarity 47.1%; Pred. No. 0.5;
Matches 16; Conservative 4; Mismatches 9; Indels 5; Gaps 3;
QY 2 HWSYGLRPGSSG--PSLQ--YIKANSKFIGITEL 31
DB 26 HWSYGLRPGKREVESLQESYAEVPE--VSFTEL 58
RESULT 10
AUT2_HUMAN
ID AUT2_HUMAN STANDARD; PRT; 1259 AA.
AC Q8WXX7; Q9Y4F2;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Autism susceptibility gene 2 protein.
DE AUT32 OR KIAA0442.
GN AUT32 OR KIAA0442.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, AND VARIANT
SER-303.
RX MEDLINE=22150863; PubMed=12160723;
RA Sultana R., Yu C.-H., Yu J., Munson J., Chen D., Hua W., Estes A.,
RA Cortes F., de la Barra F., Yu D., Haider S.T., Trask B.J., Green E.D.,
RA Raskind W.H., Distche C.M., Wijsman E., Dawson G., Storm D.R.,
RA Schellenberg G.D., Villacres E.C.;
RT "Identification of a novel gene on chromosome 7q11.2 interrupted by a
RT translocation breakpoint in a pair of autistic twins.";
RL Genomics 80:129-129(2002).
RN [2]
SEQUENCE FROM N.A. (ISOFORM 2)
RX MEDLINE=22158633; PubMed=1216954;
RA Nakajima D., Okazaki N., Yamakawa H., Kikuno R., Ohara O., Nagase T.;
RT "Construction of expression-ready cDNA clones for KIAA genes: manual
RT curation of 330 KIAA cDNA clones.";
RL DNA Res. 9:99-106(2002).
RN [3]
PRELIMINARY SEQUENCE OF 88-1259 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98116655; PubMed=9455477;
RA Ishikawa K.-I., Nagase T., Nakajima D., Seki N., Ohira M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. VIII.
RT 78 new cDNA clones from brain which code for large proteins in
RT vitro.";
RL DNA Res. 4:307-313(1997).
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Long;
CC IsoId=Q8WXX7-1; Sequence=Displayed;
CC Name=Short;
CC IsoId=Q8WXX7-2; Sequence=VSP_003792;
CC
```

CC Note-No experimental confirmation available;
 CC -!- TISSUE SPECIFICITY: Strongly expressed in brain, skeletal muscle
 CC and kidney. Also expressed in placenta, lung and leukocytes.
 CC -!- DISEASE: this gene is interrupted by a translocation breakpoint in
 CC a pair of autistic twins.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AF26917; AAL37411.1; -;
 CC DR EMBL; AB007902; BAA23714.2; ALT_INIT.
 CC DR PIR; T00065; T00065.
 CC DR Genew; HGNC:14262; AUTS2.
 CC DR MIM; 607270; -;
 CC KW Chromosomal translocation; Polymorphism; Alternative splicing.
 CC FT DOMAIN 383 410 SER-RICH.
 CC FT DOMAIN 525 548 HIS-RICH.
 CC FT DOMAIN 1122 1181 HIS-RICH.
 CC FT VARSPLIC 611 634 Missing (in isoform Short).
 CC FT VARIANT 303 303 /FTID-VSP_003792.
 CC FT VARIANT 303 303 A -> S.
 CC FT CONFLICT 177 177 /FTID-VAR_013864.
 CC FT CONFLICT 177 177 P -> S (IN REF. 2).
 CC SQ SEQUENCE 1259 AA; 138981 MW; A64D17AFF816B591 CRC64;
 CC -----
 CC Query Match 24.4%; Score 59.5; DB 1; Length 1259;
 CC Best Local Similarity 35.9%; Pred. No. 11;
 CC Matches 14; Conservative 6; Mismatches 14; Indels 5; Gaps 1;
 CC -----
 CC QY 6 GLRPGSSGSLQYIKANSKFIGITELSSG-----PSLHW 39
 CC Db 1030 GHPMKNSISLDRTRMTFPMGISPLPGGRFPYPSFW 1068
 CC -----
 CC RESULT 11
 CC GONI_MOUSE
 CC ID GONI_MOUSE STANDARD; PRT; 90 AA.
 CC AC P13562;
 CC DT 01-JAN-1990 (Rel. 13, Created)
 CC DT 01-JAN-1990 (Rel. 13, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 CC (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 CC hormone I) (GnRH I) (luliberin I); Prolactin release-inhibiting factor
 CC I].
 CC GN GNRH1 OR GNRH.
 CC OS Mus musculus (Mouse).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 CC OX NCBI_TaxID=10090;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX MEDLINE=87069928; PubMed=3024317;
 CC RA Mason A.J., Hayflick J.S., Zoeller R.T., Young W.S. III,
 CC RA Phillips H.S., Nikolic K., Seaburg P.H.;
 CC RT "A deletion truncating the gonadotropin-releasing hormone gene is
 CC responsible for hypogonadism in the tpg mouse."
 CC RL Science 234:1366-1371 (1986).
 CC CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: Belongs to the GnRH family.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M14872; AAA37717.1; -;
 CC DR PIR; A47578; RHMSG.
 CC DR MGD; MGI:95789; GnRH.
 CC DR InterPro; IPR002012; GnRH.
 CC DR InterPro; IPR004079; Gonadoliberin1.
 CC DR Pfam; PF00446; GnRH; 1.
 CC DR PRINTS; PR01541; GONADOLIBRN1.
 CC DR PROSITE; PS00473; GnRH; 1.
 CC KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Signal; Pyroglutamate carboxylic acid.
 CC FT SIGNAL 1 21
 CC FT CHAIN 22 90 PROGNADOLIBERIN I.
 CC FT PEPTIDE 22 31 GONADOLIBERIN I.
 CC FT PEPTIDE 35 90 PROLACTIN RELEASE-INHIBITING FACTOR I.
 CC FT ACT_SITE 24 24 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 CC ACTIVITY.
 CC FT MOD_RES 22 22 PYROGLUTAMATE CARBOXYLIC ACID.
 CC FT MOD_RES 31 31 AMIDATION (G-32 PROVIDE AMIDE GROUP).
 CC SQ SEQUENCE 90 AA; 10337 MW; 1C0766FAA826E4D9 CRC64;
 CC -----
 CC Query Match 24.0%; Score 58.5; DB 1; Length 90;
 CC Best Local Similarity 27.9%; Pred. No. 0.67; 17; Indels 5; Gaps 1;
 CC Matches 12; Conservative 9; Mismatches 9;
 CC QY 2 HWSYGLRPGSSGSLQYIKANSKFIGITELSSGP-----SLHW 39
 CC Db 23 HWSYGLRPGKNTLHVSFQEMGKVDQMAEPQHFECTVHW 65
 CC -----
 CC RESULT 12
 CC GONI_MACMU
 CC ID GONI_MACMU STANDARD; PRT; 67 AA.
 CC AC P55247;
 CC DT 01-OCT-1996 (Rel. 34, Created)
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 CC (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 CC hormone I) (GnRH I) (luliberin I); GnRH-associated peptide I]
 CC (Fragment).
 CC DE GNRH1 OR GNRH OR LHRH.
 CC OS Macaca mulatta (Rhesus macaque).
 CC OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 CC OC Cercopithecinae; Macaca.
 CC OX NCBI_TaxID=9544;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RX TISSUE=Hypothalamus;
 CC RX MEDLINE=95124501; PubMed=7545971;
 CC RA Ma Y.J., Costa M.E., Ojeda S.R.;
 CC RA "Developmental expression of the genes encoding transforming growth
 CC factor alpha and its receptor in the hypothalamus of female rhesus
 CC macaques."
 CC RL Neuroendocrinology 60:346-359 (1994).
 CC CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC CC -!- SUBCELLULAR LOCATION: Secreted.
 CC CC -!- SIMILARITY: Belongs to the GnRH family.
 CC -----
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 CC -----

EMBL; S75916; AAB33096.1; -.
 DR PIR; I78541;
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; Gonadoliberin1.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBERN1.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL <1 5 BY SIMILARITY.
 FT NON_TER 1 1
 FT CHAIN 6 >67 PROGNADOLIBERIN I.
 FT PEPTIDE 6 15 GONADOLIBERIN I.
 FT ACT_SITE 19 >67 GnRH-ASSOCIATED PEPTIDE I.
 FT MOD_RES 8 6 APPEARS TO BE ESSENTIAL FOR BIOLOGICAL
 FT MOD_RES 6 6 ACTIVITY (BY SIMILARITY).
 FT MOD_RES 15 15 PYRROLIDONE CARBOXYLIC ACID (BY
 FT MOD_RES 67 67 SIMILARITY).
 FT NON_TER 67 67
 FT SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;
 SQ
 Query Match 23.8%; Score 58; DB 1; Length 67;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HWSYGLRPG 10
 DB 7 HWSYGLRPG 15
 RESULT 13
 GON1_XENLA STANDARD; PRT; 89 AA.
 AC P45656;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Gonadoliberin I precursor (Gonadotropin-releasing hormone I) (GnRH-I)
 DE (LH-RH) (Luliberin I).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
 OC Xenopodinae; Xenopus.
 OC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Forebrain;
 RX MEDLINE=94185563; PubMed=8137750;
 RA Hayes W.P., Wray S., Batey J.F.;
 RT "The frog gonadotropin-releasing hormone-I (GnRH-I) gene has a
 RT mammalian-like expression pattern and conserved domains in
 RT GnRH-associated peptide, but brain onset is delayed until
 RT metamorphosis."
 RL Endocrinology 134:1835-1844(1994).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 DR EMBL; L28040; AAA49728.1; -.
 DR PIR; I51423; I51423.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; Gonadoliberin1.
 DR Pfam; PF00446; GnRH; 1.

DR PRINTS; PR01541; GONADOLIBERN1.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Signal; Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23
 FT CHAIN 24 89 PROGNADOLIBERIN I.
 FT PEPTIDE 24 33 GONADOLIBERIN I.
 FT PEPTIDE 37 89 GONADOTROPIN-RELEASING HORMONE ASSOCIATED
 FT PEPTIDE PEPTIDE.
 FT PEPTIDE 37 85 GnRH-ASSOCIATED PEPTIDE I (GAP).
 FT MOD_RES 24 24 PYRROLIDONE CARBOXYLIC ACID.
 FT MOD_RES 33 33 AMIDATION (G-34 PROVIDE AMIDE GROUP).
 SQ SEQUENCE 89 AA; 10246 MW; 6F4F36FBAE0D4284 CRC64;
 Query Match 23.8%; Score 58; DB 1; Length 89;
 Best Local Similarity 100.0%; Pred. No. 0.77;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HWSYGLRPG 10
 DB 25 HWSYGLRPG 33
 RESULT 14
 GON1_PIG STANDARD; PRT; 91 AA.
 AC P49921;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
 DE Progonadoliberin I precursor (Contains: Gonadoliberin I (LH-RH I)
 DE (luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I].
 GN GnRH1 OR GnRH.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OC NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RA Weesner G.D., Matteri R.L., Becker B.A.;
 RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 24-33.
 RX MEDLINE=72114303; PubMed=4946067;
 RA Baba Y., Matsuo H., Schally A.V.;
 RT "Structure of the porcine LH- and FSH-releasing hormone. II.
 RT Confirmation of the proposed structure by conventional sequential
 RT analyses."
 RL Biochem. Biophys. Res. Commun. 44:459-463(1971).
 RN [3]
 RP SYNTHESIS OF GONADOLIBERIN.
 RX MEDLINE=72065376; PubMed=4942726;
 RA Matsuo H., Arimura A., Nair R.M.G., Schally A.V.;
 RT "Synthesis of the porcine LH- and FSH-releasing hormone by the solid-
 RT phase method."
 RL Biochem. Biophys. Res. Commun. 45:822-827(1971).
 RN [4]
 RP SYNTHESIS OF GONADOLIBERIN.
 RX MEDLINE=72117544; PubMed=4946275;
 RA Baba Y., Arimura A., Schally A.V.;
 RT "On the tryptophan residue in porcine LH and FSH-releasing hormone."
 RL Biochem. Biophys. Res. Commun. 45:483-487(1971).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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EMBL; L32864; AAA31066.1; -
 InterPro: IPR002012; GnRH.
 InterPro: IPR004079; Gonadoliberin I.
 Pfam: PF00446; GnRH; 1
 PRINTS; PR01541; GONADOLIBERNI.
 PROSITE; PS00473; GnRH; 1.
 Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 Placenta; Signal; Pyrrolidone carboxylic acid.
 SIGNAL 1 23
 CHAIN 24 91
 PEPTIDE 24 33
 ACT_SITE 26 91
 MOD_RES 24 24
 MOD_RES 33 33
 SEQUENCE 91 AA; 10090 MW; 8340474F32DDAA99 CRC64;
 Query Match 23.8%; Score 58; DB 1; Length 91;
 Best Local Similarity 100.0%; Pred. No. 0.79; Indels 0; Gaps 0;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 2 HWSYGLRPG 10
 25 HWSYGLRPG 33

RESULT 15
 GONI HUMAN STANDARD; PRT; 92 AA.
 AC P01148;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I) (Gonadorelin); GnRH-associated
 DE peptide I].
 OS GnRH OR GnRH OR LHRH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8936682; PubMed=2671939;
 RA Hayflick J.S., Adelman J.P., Seeburg P.H.;
 RT "The complete nucleotide sequence of the human gonadotropin-releasing
 RT hormone gene.";
 RL Nucleic Acids Res. 17:6403-6403(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094338; PubMed=2867548;
 RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
 RT "Isolation of the gene and hypothalamic cDNA for the common precursor
 RT of gonadotropin-releasing hormone and prolactin release-inhibiting
 RT factor in human and rat.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:179-183(1986).
 RN [3]
 RP SEQUENCE FROM N.A., AND VARIANT SER-16.
 RX MEDLINE=85012739; PubMed=6030951;
 RA Seeburg P.H., Adelman J.P.;
 RT "Characterization of cDNA for precursor of human luteinizing hormone
 RT releasing hormone.";
 RL Nature 311:666-668(1984).
 RN [4]
 RP SEQUENCE OF 24-33.
 RX MEDLINE=83126573; PubMed=6760865;

Tan L., Rousseau P.;
 "The chemical identity of the immunoreactive LHRH-like peptide
 biosynthesized in the human placenta";
 Biochem. Biophys. Res. Commun. 109:1061-1071(1982).
 [5]
 VARIANT SER-16.
 MEDLINE=99318093; PubMed=10391209;
 Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes.";
 Nat. Genet. 22:231-238(1999).
 [6]
 ERRATUM.
 Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaraman N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 Nat. Genet. 23:373-373(1999).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
 CC Lutrepulse or Lutrelief (Ferring Pharmaceuticals) and Relisorm
 CC (Seronol).
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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EMBL; X01059; CAA25526.1; -
 EMBL; M12578; AAA35916.1; -
 EMBL; X15215; CAA33285.1; -
 PIR; S05308; RHUG.
 Genew; HGNC:4419; GnRH1.
 MIM; 152760; -
 GO; GO:0005625; C:soluble fraction; TAS.
 GO; GO:0005183; F:luteinizing hormone-releasing factor activity; TAS.
 GO; GO:0007267; P:cell-cell signaling; TAS.
 GO; GO:0007275; P:development; TAS.
 GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 GO; GO:0007165; P:signal transduction; TAS.
 InterPro: IPR002012; GnRH.
 InterPro: IPR004079; Gonadoliberin I.
 Pfam: PF00446; GnRH; 1.
 PRINTS; PR01541; GONADOLIBERNI.
 PROSITE; PS00473; GnRH; 1.
 Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 Placenta; Pharmaceutical; Signal; Polymorphism;
 Pyrrolidone carboxylic acid.
 SIGNAL 1 23
 CHAIN 24 92
 PEPTIDE 24 33
 ACT_SITE 26 26
 MOD_RES 24 24
 MOD_RES 33 33
 VARIANT 16 16
 SEQUENCE 92 AA; 10380 MW; 30A72221E076FA79 CRC64;
 Query Match 23.8%; Score 58; DB 1; Length 92;
 Best Local Similarity 100.0%; Pred. No. 0.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-09-848-834a-19.open.rsp

Wed Mar 10 10:34:29 2004

Qv 2 HWSYCLRPG 10
| | | | |
Db 25 HWSYCLRPG 33

Search completed: March 10, 2004, 09:13:59
Job time : 9.41245 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 45.463 Seconds
(without alignments)
319.245 Million cell updates/sec

Title: US-09-848-834A-19
Perfect score: 244
Sequence: 1 XHWSYGLRPGSSGSLQYIK.....GITESSGSLHWSYGLRXP 46

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database : SPTREMBL 25:*
- 1: sp_archea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phase:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_virus:*
 - 16: sp_bacteriap:*
 - 17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	31.1	1310	Q93N27	Q93N27 clostridium
2	71	29.1	1331	Q9SF03	Q9SF03 arabisidopsis
3	71	29.1	1379	Q84R20	Q84R20 arabisidopsis
4	67	27.5	7223	Q7URP6	Q7URP6 rhodopirell
5	64	26.2	82	Q30VY3	Q30VY3 oncorhynch
6	63	25.8	82	Q30VY3	Q30VY3 oncorhynch
7	62.5	25.6	329	Q7TQ24	Q7TQ24 rattus norv
8	61	25.0	458	Q9A409	Q9A409 caulobacter
9	61	25.0	1019	Q7XBC5	Q7XBC5 viscum albu
10	60	24.6	447	Q91504	Q91504 pseudomonas
11	59	24.2	91	Q3PRH0	Q3PRH0 anguilla ja
12	59	24.2	366	Q8N0N3	Q8N0N3 penaeus mon
13	59	24.2	385	Q9Z201	Q9Z201 cavia porce
14	59	24.2	473	Q8VUQ1	Q8VUQ1 pseudomonas
15	59	24.2	475	Q88Q03	Q88Q03 pseudomonas
16	58.5	24.0	164	Q86D87	Q86D87 ciona intes

17	58.5	24.0	165	5	Q86D88	Q86D88 ciona intes
18	58.5	24.0	329	4	Q96SA1	Q96SA1 homo sapien
19	58.5	24.0	329	4	Q96P93	Q96P93 homo sapien
20	58.5	24.0	329	4	Q8WZ19	Q8WZ19 homo sapien
21	58.5	24.0	374	16	Q92VR6	Q92VR6 rhizobium m
22	58.5	24.0	447	16	Q8R756	Q8R756 thermocanaer
23	57	23.4	192	10	Q8LGA9	Q8LGA9 arabisidopsis
24	57	23.4	530	10	Q9XID7	Q9XID7 arabisidopsis
25	56.5	23.2	329	11	Q8BGV7	Q8BGV7 mus musculus
26	56.5	23.2	467	2	Q8KTE3	Q8KTE3 methylobact
27	56	23.0	439	4	Q8IYV0	Q8IYV0 homo sapien
28	55.5	22.7	229	5	Q8SR88	Q8SR88 encephalito
29	55	22.5	165	2	Q8L2C0	Q8L2C0 proteus vul
30	55	22.5	289	16	Q889H0	Q889H0 rhizobium 1
31	55	22.5	364	10	Q9LDE6	Q9LDE6 arabisidopsis
32	55	22.5	376	5	Q8MVS9	Q8MVS9 litoranacae
33	55	22.5	417	16	Q9PGX9	Q9PGX9 xylella fas
34	55	22.5	417	16	Q87F07	Q87F07 xylella fas
35	55	22.5	447	16	Q7VQH3	Q7VQH3 candidatus
36	55	22.5	871	5	Q44358	Q44358 nephila cla
37	55	22.5	2249	5	Q9NHM4	Q9NHM4 nephila cla
38	54.5	22.3	124	4	Q8N9W7	Q8N9W7 homo sapien
39	54.5	22.3	152	16	Q88AX1	Q88AX1 pseudomonas
40	54.5	22.3	204	16	Q8PHA4	Q8PHA4 xanthomonas
41	54.5	22.3	219	5	Q86D90	Q86D90 ciona intes
42	54.5	22.3	219	5	Q86D89	Q86D89 ciona intes
43	54.5	22.3	355	16	Q8R831	Q8R831 thermocanaer
44	54.5	22.3	435	12	Q9WPM1	Q9WPM1 bluetongue
45	54.5	22.3	929	4	Q8NGZ7	Q8NGZ7 homo sapien

ALIGNMENTS

RESULT 1

Q93N27 PRELIMINARY; PRT; 1310 AA.

ID Q93N27; DT 01-DEC-2001 (TREMREL. 19, Created)
DT 01-DEC-2001 (TREMREL. 19, Last sequence update)
DT 01-OCT-2003 (TREMREL. 25, Last annotation update)
DE Tetanus toxin (Fragment).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RA Shumin Z., Dianliang L.;
RT "Cloning and sequence analysis of tetanus toxin gene";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF389424; AAK72964.2; -
DR GO; GO:0004866; F:Endopeptidase inhibitor activity; IEA.
DR GO; GO:0008237; F:metallopeptidase activity; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0009405; P:proteolysis and peptidolysis; IEA.
DR GO; GO:0008508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR008985; ConsAlike_1ec_g1.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002160; Kunitz legume.
DR InterPro; IPR000395; Peptidase M27.
DR InterPro; IPR006025; Pept M Zn_BS.
DR Pfam; PF01742; Peptidase M27.
DR PRINTS; PR00760; BONTOXILYSIN.
DR PRODOM; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00225; CRYSTALLIN BETAGAMMA; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
DR NON_TER 1
FT NON_TER 1310 1310
SQ SEQUENCE 1310 AA; 150316 MW; 9EADD914418E450 CRC64;

Query Match

31.1%; Score 76; DB 2; Length 1310;

Best Local Similarity 93.8%; Pred. No. 0.59; Mismatches 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LQYKANSKFIGITEL 31
DB 830 MQYKANSKFIGITEL 845

RESULT 2

Q9SF03 Q9SF03 PRELIMINARY; PRT; 1331 AA.
AC Q9SF03;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE F26K24.25 protein (Genomic DNA, chromosome 3, P1 clone: MEC18).
GN F26K24.25
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucotsids II; Brassicales; Brassicaceae; Arabidopsais.
OC NCBI_TaxID=3702;
RN SEQUENCE FROM N.A.
RP STRAIN=cv. Columbia;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
RA Rensing C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Nierman W.C., Fraser C.M.;
RA "Arabidopsis thaliana chromosome III BAC F26K24 genomic sequence."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX PubMed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the regions of 4,251,695 bp covered by ninety P1,
RT TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL; AC016795; AAF2312.1; -;
DR EMBL; AP002040; BAB03106.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPSP_A.C.
DR Pfam; PF03178; CPSP_A; 1.
SQ SEQUENCE 1331 AA; 146497 MW; 2979F40E8975143E CRC64;

Query Match 29.1%; Score 71; DB 10; Length 1331;
Best Local Similarity 36.1%; Pred. No. 2.8; Mismatches 9; Indels 2; Gaps 1;
Matches 13; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 4 SYGLRPGSGPSLQYKANSKFIGI--TELSSGSPSL 37
DB 904 SYKLPGETGKSMELVRVGNHVLVVGTSLSGGPAI 939

RESULT 3

Q84R20 Q84R20 PRELIMINARY; PRT; 1379 AA.
AC Q84R20;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein At3g11960.
GN At3g11960.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;

OC eucotsids II; Brassicales; Brassicaceae; Arabidopsais.

QY NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Hsuan V.W., Lee J.M.,
RA Onodera C.S., Quach H.L., Tang C., Toriumi M., Wong C., Wu H.C.,
RA Yu G., Yuan S., Carninci P., Chen H., Cheuk R., Hayashizaki Y.,
RA Ishida J., Jones T., Kamiya A., Kawai J., Kim C.J., Narusaka M.,
RA Nguyen M., Palm C.J., Sakurai T., Satou M., Seki M., Shinn P.,
RA Southwick A., Tripp M.G., Wu T., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RT "Arabidopsis Full Length cDNA Clones."
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BT006164; AAP04148.1; -;
DR GO; GO:0005634; C:nucleus; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR InterPro; IPR004871; CPSP_A.C.
DR InterPro; IPR007087; Znf_C2H2.
DR Pfam; PF03178; CPSP_A; 1.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 1.
KW Hypothetical protein.
SQ SEQUENCE 1379 AA; 151853 MW; 451A0B63797F7D92 CRC64;

Query Match 29.1%; Score 71; DB 10; Length 1379;
Best Local Similarity 36.1%; Pred. No. 2.9; Mismatches 9; Indels 2; Gaps 1;
Matches 13; Conservative 12; Mismatches 9; Indels 2; Gaps 1;

QY 4 SYGLRPGSGPSLQYKANSKFIGI--TELSSGSPSL 37
DB 952 SYKLPGETGKSMELVRVGNHVLVVGTSLSGGPAI 987

RESULT 4

Q7URP6 Q7URP6 PRELIMINARY; PRT; 7223 AA.
AC Q7URP6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB5524
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OC NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RC MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
RL EMBL; BX294142; CAD74292.1; -;
RW Hypothetical protein; Complete proteome.
SQ SEQUENCE 7223 AA; 767506 MW; 0031D53A0B28139A CRC64;

Query Match 27.5%; Score 67; DB 16; Length 7223;
Best Local Similarity 42.3%; Pred. No. 69; Mismatches 22; Conservative 6; Mismatches 12; Indels 12; Gaps 4;

QY 3 WSYGLRPGSGSP---SLQYIK---ANSKFIGITE-----LSSGSPSLHWSYGL 43
DB 2531 WYFGLTWDSPANGSKYLNPAAGNNOF-GITEVQHADLSSNPSSNLSYDL 2581

RESULT 5

Q90VY3 Q90VY3 PRELIMINARY; PRT; 82 AA.
AC Q90VY3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002886; Peptidase_M37.
 DR Pfam: PF01551; Peptidase_M37; I.
 DR Complete proteome.
 KW SEQUENCE 458 AA; 49491 MW; C477081FE97BEA24 CRC64;

Query Match 25.0%; Score 61; DB 16; Length 458;
 Best Local Similarity 31.0%; Pred. No. 16;
 Matches 13; Conservative 11; Mismatches 14; Indels 4; Gaps 1;

QY 3 WSYGLRPGSSPSLOYIKANSKFICITELSSGSPSLHWSYGLR 44
 DB 357 YAKGIKPGTRVRRQGVV----AYVGSTGMSSGPHLHYEVWLK 394

RESULT 9

Q7XBC5 PRELIMINARY; PRT; 1019 AA.
 AC Q7XBC5;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Sucrose phosphate synthase.
 OS Viscum album subsp. album.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Santalales; Santalaceae; Viscum.
 OX NCBI_TaxID=104253;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Maenner P., Hamp R.F.;
 RT "Sucrose phosphate synthase from mistletoe (Viscum album ssp.
 album)".;
 RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY331261; AAP94624.1; -;
 SQ SEQUENCE 1019 AA; 114142 MW; 3F81900921FC3CD3 CRC64;

Query Match 25.0%; Score 61; DB 10; Length 1019;
 Best Local Similarity 26.7%; Pred. No. 42;
 Matches 12; Conservative 9; Mismatches 14; Indels 10; Gaps 1;

QY 8 RFGSSGPSLOYIKANSKFICITELSSGSPSLHWSY 42
 DB 182 RSDTGGQVKYVELARALGTMPIGYRVDLTLTQVSPADIHWSY 226

RESULT 10

Q915Q4 PRELIMINARY; PRT; 447 AA.
 AC Q915Q4;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein PA0667.
 GN PA0667.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RA MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufragile W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen."
 RL Nature 406:959-964 (2000).
 DR EMBL; AE004501; AAG04056.1; -;

DR PIR; B83563; B83563.
 DR GO: GO:0004222; P:metalloendopeptidase activity; IEA.
 DR GO: GO:0006508; P:proteolysis and peptidolysis; IEA.
 DR InterPro: IPR002886; Peptidase_M37.
 DR Pfam: PF01551; Peptidase_M37; I.
 DR Complete proteome.
 KW SEQUENCE 447 AA; 49156 MW; 5E33C252C2C8CD9D CRC64;

Query Match 24.6%; Score 60; DB 16; Length 447;
 Best Local Similarity 36.1%; Pred. No. 21;
 Matches 13; Conservative 9; Mismatches 10; Indels 4; Gaps 1;

QY 6 GLRPGSSGPSLOYIKANSKFICITELSSGSPSLHWSY 41
 DB 363 GIRAGTSVKQGOII----GYVGMTGLATGPHLHYEF 394

RESULT 11

Q9PRH0 PRELIMINARY; PRT; 91 AA.
 AC Q9PRH0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Prepro-mGnRH precursor (Gonadoliberin) (Gonadotropin-releasing
 hormone) (LH-RH) (Luliberin).
 OS Anguilla japonica (Japanese eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7937;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Okubo K., Suetake H., Aida K.;
 RT "Expression of two gonadotropin-releasing hormone (GnRH) precursor
 genes in various tissues of the Japanese eel and evolution of GnRH.";
 RL Zool. Sci. 16:471-478 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Okubo K., Suetake H., Aida K.;
 RT "A splicing variant for the prepro-mammalian gonadotropin-releasing
 hormone (prepro-mGnRH) mRNA is present in the brain and various
 peripheral tissues of the Japanese eel.";
 RL Zool. Sci. 16:645-651 (1999).
 CC -1- FUNCTION: STIMULATES THE SECRETION OF GONADOTROPINS (BY
 SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GnRH FAMILY.
 DR EMBL; AB026589; BAA83608.1; -;
 DR EMBL; AB026591; BAA83597.1; -;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0005183; F:lutetizing hormone-releasing factor activity; IEA.
 DR GO: GO:0007275; P:development; IEA.
 DR InterPro: IPR002012; GnRH.
 DR InterPro: IPR004079; Gonadoliberin.
 DR Pfam: PF00446; GnRH; 1.
 DR PRINTS; PR01541; GONADOLIBERN1.
 DR PROSITE; PS00473; GnRH; 1.
 DR Amidation; Hormone; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 32
 FT CHAIN 33 91
 SQ SEQUENCE 91 AA; 9893 MW; BA15C9DC08434A7B CRC64;

Query Match 24.2%; Score 59; DB 13; Length 91;
 Best Local Similarity 66.7%; Pred. No. 4.4;
 Matches 12; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 2 HWSYGLRPGS--SGPSIQ 17
 DB 24 HWSYGLRPGKRGADSIQ 41

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RESULT 12
Q8N0N3 PRELIMINARY; PRT; 366 AA.
ID Q8N0N3
AC Q8N0N3
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Beta-1,3-glucan binding protein.
OS Peneaus monodon (Peneid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE FROM N.A.
RA Sriunyaluckana K., Lee S.Y., Soderhall K.;
RT "The beta-1,3-glucan binding protein from the black tiger shrimp,
RT Peneaus monodon."
RL Submitted (APR-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF368168; AAM1213.1;
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . . ; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR008985; ConA-like_lectgl.
DR InterPro; IPR000757; Glyco_hydro_16.
DR Pfam; PF00722; Glyco_hydro_16; 1.
SQ SEQUENCE 366 AA; 41497 MW; 6F540A0E83FDD7D CRC64;

Query Match 24.2%; Score 59; DB 5; Length 366;
Best Local Similarity 31.6%; Pred. No. 23;
Matches 12; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGSPSLQYIKANSKFIGITELSSGSPSLHW 39
Db 171 NWPYGLWPASGEIDILESGRGNDDFGTGLGNQYGGTTLHW 208

RESULT 13
Q9Z201 PRELIMINARY; PRT; 385 AA.
ID Q9Z201
AC Q9Z201;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-OCT-2002 (TReMBLrel. 22, Last annotation update)
DE Fibrogen A-alpha chain (fragment).
OS Cavia porcellus (Guinea pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.
OX NCBI_TaxID=10141;
RN [1]
RP SEQUENCE FROM N.A.
RA Murakawa M.;
RL Submitted (SEP-1998) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AF095466; AAC67565.1;
DR HSSP; P02671; 1F2F.
FT NON TER 1
FT NON TER 385
SQ SEQUENCE 385 AA; 40909 MW; FA576CA0E2A2101A CRC64;

Query Match 24.2%; Score 59; DB 11; Length 385;
Best Local Similarity 38.1%; Pred. No. 24;
Matches 16; Conservative 2; Mismatches 12; Indels 12; Gaps 2;

QY 2 HWSYGLRPGSSGSPSLQYIKANSKFIGITELSSGSPSLHWYGL 43
Db 128 HWI----PSSGPGSQDPVSS-----PSSGSGHWSSGV 157

RESULT 14
Q8VUQ1 PRELIMINARY; PRT; 473 AA.
ID Q8VUQ1
AC Q8VUQ1
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)

RESULT 15
Q88QQ3 PRELIMINARY; PRT; 475 AA.
ID Q88QQ3
AC Q88QQ3;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Peptidase, M23/M37 family.
GN PP0435.
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA Madupu R., Nelson W., White O., Paterson J., Khouri H., Hance I.,
RA Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA Unterback T., Rizzo M., Lee K., Kosack D., Noesti D., Wedler H.,
RA Lauber J., Stjepandic D., Hohnselt J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440."
RL Environ. Microbiol. 4:799-808(2002).
DR EMBL; AS016775; AAN6065.1;
DR TIGR; PP0435;
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M37.
DR Pfam; PF01551; Peptidase_M37; 1.
KW Complete proteome.
SQ SEQUENCE 475 AA; 51663 MW; 9D816AB099E05A31 CRC64;

Query Match 24.2%; Score 59; DB 16; Length 475;
Best Local Similarity 38.9%; Pred. No. 31;
Matches 14; Conservative 7; Mismatches 11; Indels 4; Gaps 1;

QY 6 GLRPGSSGSPSLQYIKANSKFIGITELSSGSPSLHWY 41
Db 390 GIKTGSTVKQGI---GYIGTGTGLSTGPHLHYEF 421

01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Toluene resistance protein Trg3.
GN TRG3.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KT2442;
RA Fukumori F., Kishii M.;
RT "Characterization of the toluene-sensitive mutants of Pseudomonas
RT putida KT2442TOL."
RL Submitted (JUL-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AB066296; BAB3598.1;
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR002886; Peptidase_M37.
DR Pfam; PF01551; Peptidase_M37; 1.
SQ SEQUENCE 473 AA; 51435 MW; CCB7BFA918C1039 CRC64;

Query Match 24.2%; Score 59; DB 2; Length 473;
Best Local Similarity 38.9%; Pred. No. 31;
Matches 14; Conservative 7; Mismatches 11; Indels 4; Gaps 1;

QY 6 GLRPGSSGSPSLQYIKANSKFIGITELSSGSPSLHWY 41
Db 390 GIKTGSTVKQGI---GYIGTGTGLSTGPHLHYEF 421

```


Db 392 GIKTGSTVKQOII-----GYIGTTGLSTGPHLYEF 423

Search completed: March 10, 2004, 09:25:41
Job time : 47.463 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48 ; Search time 69.2685 Seconds
(without alignments)
187.635 Million cell updates/sec

Title: US-09-848-834A-19
Perfect score: 244
Sequence: 1 XHWSYGLRPGSGPSLYIK.....GITESSGSLHWSYGLRXP 46

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: Geneseq1980s:*
2: Geneseq1990s:*
3: Geneseq2000s:*
4: Geneseq2001s:*
5: Geneseq2002s:*
6: Geneseq2003as:*
7: Geneseq2003bs:*
8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	242	99.2	46	5	AAU11430	AAU11430 Synthetic
2	161	66.0	31	5	AAU11426	AAU11426 Synthetic
3	160.5	65.8	51	5	AAU11431	AAU11431 Synthetic
4	147.5	60.5	47	5	AAU11428	AAU11428 Synthetic
5	145	59.4	50	5	AAU11429	AAU11429 Synthetic
6	136	55.7	28	5	AAU11422	AAU11422 Synthetic
7	114.5	46.9	47	2	AAE62723	AAE62723 LHRH-cont
8	113.5	46.5	27	2	AAE62701	AAE62701 LHRH-cont
9	113.5	46.5	27	7	ADD89947	ADD89947 LHRH pept
10	108.5	44.5	695	2	AAW79573	AAW79573 LKT-GnRH
11	108.5	44.5	695	3	AAW58361	AAW58361 Leukotoxi
12	108.5	44.5	695	3	AAW58133	AAW58133 Gonadotro
13	106	43.4	49	2	AAW03944	AAW03944 GnRH 4-re
14	106	43.4	49	2	AAW79567	AAW79567 GnRH-2, 1
15	106	43.4	49	2	AAW61542	AAW61542 Peptide h
16	106	43.4	49	3	AAW58363	AAW58363 Four-copy
17	106	43.4	49	3	AAW58135	AAW58135 GnRH anal
18	106	43.4	544	2	AAW03943	AAW03943 LKT-GnRH
19	106	43.4	544	2	AAW79570	AAW79570 LKT-GnRH
20	106	43.4	977	2	AAW03942	AAW03942 LKT-GnRH
21	106	43.4	977	2	AAW79569	AAW79569 LKT-GnRH
22	94	38.5	42	3	AAW79565	AAW79565 GnRH tand
23	92.5	37.9	23	3	AAE20865	AAE20865 GnRH tand
24	91	37.3	30	2	AAW03923	AAW03923 Luteinisi
25	91	37.3	40	2	AAW31183	AAW31183 Ubiquitin

26	91	37.3	40	4	AAW71954	AAW71954 GnRH sequ
27	91	37.3	41	2	AAW31182	AAW31182 Ubiquitin
28	91	37.3	41	4	AAW71953	AAW71953 GnRH sequ
29	90	36.9	40	3	AAW96085	AAW96085 Cattle go
30	90	36.9	283	2	AAW11186	AAW11186 Plasmid p
31	90	36.9	323	2	AAW11187	AAW11187 Plasmid p
32	90	36.9	398	3	AAW96090	AAW96090 BHV-1 tru
33	90	36.9	399	3	AAW96093	AAW96093 BHV-1 tru
34	90	36.9	411	3	AAW96089	AAW96089 GnRH tetr
35	90	36.9	442	3	AAW96091	AAW96091 GnRH tetr
36	89	36.5	34	5	AAU11424	AAU11424 Synthetic
37	89	36.5	36	5	AAU11427	AAU11427 Synthetic
38	89	36.5	216	3	AAW92665	AAW92665 MUC-1 ana
39	89	36.5	750	3	AAW92638	AAW92638 Mutant hu
40	88	36.1	221	5	ABW76114	ABW76114 PEIA-GnRH
41	88	36.1	537	7	ABR82481	ABR82481 Truncated
42	88	36.1	713	7	ABR82480	ABR82480 Modified
43	87	35.7	20	2	AAW47438	AAW47438 Antigenic
44	87	35.7	20	2	AAW31174	AAW31174 Ubiquitin
45	87	35.7	20	2	AAW31177	AAW31177 Ubiquitin

ALIGNMENTS

RESULT 1	
ID	AAU11430
XX	AAU11430 standard; peptide; 46 AA.
AC	AAU11430;
XX	
DT	12-MAR-2002 (first entry)
XX	
DE	Synthetic immunogen peptide 11.
XX	
KW	Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
KW	luteinising hormone releasing hormone; LHRH; contraceptive;
KW	promiscuous helper T-cell peptide epitope; immunomic peptide epitope;
KW	breast cancer; uterine cancer; gynaecological cancer; endometriosis;
KW	uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX	
OS	Clostridium tetani.
OS	Mammalia.
OS	Synthetic.
OS	Chimeric.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1. .10
FT	/note= "Gonadotrophin releasing hormone epitope (1. .10 aa)"
FT	Misc-difference
FT	/label= OTHER
FT	/note= "Other= Pyro-glutamic acid or 5-oxo proline"
FT	Peptide
FT	11. .16
FT	/note= "Spacer peptide"
FT	Peptide
FT	17. .31
FT	/note= "Tetanus toxoid (830-844 aa)"
FT	Peptide
FT	32. .37
FT	/note= "Spacer peptide"
FT	Peptide
FT	38. .46
FT	/note= "Gonadotrophin releasing hormone epitope (2-10 aa)"
FT	Modified-site
FT	46
FT	/note= "Amidated glycine or glycineamide"
XX	
XX	WC200185763-A2.
PN	
XX	
XX	15-NOV-2001.
PD	
XX	
XX	04-MAY-2001; 2001WO-US014363.
PF	
XX	
XX	05-MAY-2000; 2000US-0202328P.
PR	
XX	

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PA (APHT-) APHTON CORP.
XX Grimes S, Michaeli D, Stevens VC;
XX WPI; 2002-049440/06.
XX Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX Claim 11; Page 12; 43pp; English.
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH) also known as
XX luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX
XX Sequence 46 AA;
XX
XX Query Match 99.2%; Score 242; DB 5; Length 46;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-23;
XX Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 HWSYGLRPGSSGSPSLQYIKANSKFGITELSGPSLHWSYGLRP 45
XX
XX Db 2 HWSYGLRPGSSGSPSLQYIKANSKFGITELSGPSLHWSYGLRP 45
XX
XX RESULT 2
XX AAU11426
XX ID AAU11426 standard; peptide; 31 AA.
XX
XX AC AAU1426;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Synthetic immunogen peptide 7.
XX
XX KW Gonadotropin releasing hormone; GnRH; synthetic immunogen;
XX luteinising hormone releasing hormone; LHRH; contraceptive;
XX promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
XX breast cancer; uterine cancer; gynaecological cancer; endometriosis;
XX uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX
XX OS Clostridium tetani.
XX OS Mammalia.
XX OS Synthetic.
XX OS Chimeric.
XX
XX XX Key Location/Qualifiers
XX FH Peptide 1. .10
XX FT /note= "Gonadotropin releasing hormone epitope"
XX FT Misc-difference 1
XX FT /label= OTHER
XX FT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
XX FT Peptide 11. .16
XX FT /note= "Spacer peptide"
XX FT Peptide 17. .31
XX FT /note= "Tetanus toxoid sequence (830-844 aa)"
XX
XX W0200185763-A2.
XX
XX PN 15-NOV-2001.
XX
XX PD
XX
XX

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PF 04-MAY-2001; 2001WO-US014363.
XX
XX PR 05-MAY-2000; 2000US-0202328P.
XX
XX PA (APHT-) APHTON CORP.
XX
XX PI Grimes S, Michaeli D, Stevens VC;
XX
XX PX WPI; 2002-049440/06.
XX
XX DR Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX Claim 11; Page 10; 43pp; English.
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH) also known as
XX luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX
XX Sequence 31 AA;
XX
XX Query Match 66.0%; Score 161; DB 5; Length 31;
XX Best Local Similarity 100.0%; Pred. No. 1.8e-13;
XX Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 2 HWSYGLRPGSSGSPSLQYIKANSKFGITEL 31
XX
XX Db 2 HWSYGLRPGSSGSPSLQYIKANSKFGITEL 31
XX
XX RESULT 3
XX AAU11431
XX ID AAU11431 standard; peptide; 51 AA.
XX
XX AC AAU1431;
XX
XX DT 12-MAR-2002 (first entry)
XX
XX DE Synthetic immunogen peptide 12.
XX
XX KW Gonadotropin releasing hormone; GnRH; synthetic immunogen;
XX luteinising hormone releasing hormone; LHRH; contraceptive;
XX promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
XX breast cancer; uterine cancer; gynaecological cancer; endometriosis;
XX uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX
XX OS Plasmodium falciparum.
XX OS Mammalia.
XX OS Synthetic.
XX OS Chimeric.
XX
XX XX Key Location/Qualifiers
XX FH Peptide 1. .10
XX FT /note= "Gonadotropin releasing hormone epitope (1. .10
XX FT aa)"
XX FT Misc-difference 1
XX FT /label= OTHER
XX FT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
XX FT Peptide 11. .16
XX FT /note= "Spacer peptide"
XX FT Peptide 17. .36
XX FT /note= "Malaria CSP protein (378-398 aa)"
XX

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FT Peptide 37..42
FT /note= "Spacer peptide"
FT Peptide 43..51
FT /note= "Gonadotrophin releasing hormone epitope (2-10
FT aa)"
FT Modified-site 51
FT /note= "Amidated glycine or glycineamide"
XX WO200185763-A2.
XX 15-NOV-2001.
XX 04-MAY-2001; 2001WO-US014363.
XX 05-MAY-2000; 2000US-0202328P.
XX (APHT-) APHTON CORP.
XX Grimes S, Michaeli D, Stevens VC;
XX WPI; 2002-049440/06.
XX Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX Claim 11; Page 12-13; 43pp; English.
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH) also known as
XX luteinising hormone releasing hormone, (LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX Sequence 51 AA;
XX Query Match 65.8%; Score 160.5; DB 5; Length 51;
XX Best Local Similarity 66.0%; Pred. No. 3.9e-13;
XX Matches 33; Conservative 3; Mismatches 7; Indels 7; Gaps 2;
QY 2 HWSYGLRPGSSGPSL-----QYIKANSKFGICITELSSGSPSLHWSYGLRP 45
DB 2 HWSYGLRPGSSGPSLDEKIKAKWEKASSVF-NVNVSSSGPSLHWSYGLRP 50
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 4
AAU11428
ID AAU11428 standard; peptide; 47 AA.
AC AAU11429;
XX AAU11429;
DT 12-MAR-2002 (first entry)
XX Synthetic immunogen peptide 9.
DE Gonadotropin releasing hormone; GnRH; synthetic immunogen;
XX luteinising hormone releasing hormone; LHRH; contraceptive;
KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX Plasmodium falciparum.
OS Mammalia.
OS Synthetic.
OS Chimeric.

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XX Key Location/Qualifiers
XX Peptide 1..10
XX /note= "Gonadotrophin releasing hormone epitope (1..10
XX aa)"
XX Misc-difference 1
XX /label= OTHER
XX Peptide 11..16
XX /note= "Other= Pyro-glutamic acid or 5-oxo proline"
XX /note= "Spacer peptide"
XX Peptide 17..34
XX /note= "Malaria CSP protein (288-302 aa)"
XX Peptide 35..38
XX /note= "Spacer peptide"
XX Peptide 39..47
XX /note= "Gonadotrophin releasing hormone epitope (2-10
XX aa)"
XX Modified-site 47
XX /note= "Amidated glycine or glycineamide"
XX WO200185763-A2.
XX 15-NOV-2001.
XX 04-MAY-2001; 2001WO-US014363.
XX 05-MAY-2000; 2000US-0202328P.
XX (APHT-) APHTON CORP.
XX Grimes S, Michaeli D, Stevens VC;
XX WPI; 2002-049440/06.
XX Novel synthetic immunogen for inducing immune response against
XX gonadotropin releasing hormone, comprises fusion peptide having
XX promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
XX or its analog.
XX Claim 11; Page 11; 43pp; English.
XX The invention relates to a synthetic immunogen for inducing specific
XX antibodies against gonadotropin releasing hormone (GnRH) also known as
XX luteinising hormone releasing hormone, (LHRH) comprising a fusion peptide
XX which comprises a promiscuous helper T-cell peptide epitope and
XX immunomimic peptide epitope or its analogue. The synthetic immunogen is
XX useful inducing an immune response against GnRH in an animal subject, and
XX as such is useful as a contraceptive and in the treatment of diseases
XX such as cancer (of the breast, uterus and other gynaecological cancer),
XX endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX prostate cancer. The immunogen is effective in eliciting high and
XX specific anti-GnRH antibody titres. The present sequence is a synthetic
XX immunogen of the invention
XX Sequence 47 AA;
XX Query Match 60.5%; Score 147.5; DB 5; Length 47;
XX Best Local Similarity 62.5%; Pred. No. 1.6e-11;
XX Matches 30; Conservative 4; Mismatches 7; Indels 7; Gaps 2;
QY 2 HWSYGLRPGSSGSPSLQYIKANSKFGI-----TELSSGSPSLHWSYGLRP 45
DB 2 HWSYGLRPGSSGSPSLKLL---SEIKGVIVHRLEGEVGPSPSLHWSYGLRP 46
XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX
RESULT 5
AAU11429
ID AAU11429 standard; peptide; 50 AA.
XX AAU11429;
XX 12-MAR-2002 (first entry)
XX

```

DE XX Synthetic immunogen peptide 10.

KW Gonadotropin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.

XX Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Peptide 1..10
 FT /note= "Gonadotropin releasing hormone epitope (1..10 aa)"
 FT Misc-difference 1
 FT /label= OTHER
 FT /note= "Other= Pyro-glutamic acid or 5-oxo proline"
 FT Peptide 11..16
 FT /note= "Spacer peptide"
 FT Peptide 17..37
 FT /note= "Tetanus toxoid (947-967 aa)"
 FT Peptide 38..41
 FT /note= "Spacer peptide"
 FT Peptide 42..50
 FT /note= "Gonadotropin releasing hormone epitope (2-10 aa)"
 FT Modified-site 50
 FT /note= "Amidated glycine or glycineamide"

XX WO200185763-A2.
 XX 15-NOV-2001.
 XX 04-MAY-2001; 2001WO-US014363.
 XX 05-MAY-2000; 2000US-0202328P.
 XX (APHT-) APHTON CORP.
 XX Grimes S, Michaeli D, Stevens VC;
 XX WPI; 2002-049440/06.
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.

XX Claim 11; Page 11; 43pp; English.

CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone (LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention

XX Sequence 50 AA;
 SQ

Query Match 59.4%; Score 145; DB 5; Length 50;
 Best Local Similarity 60.4%; Pred. No. 3.7e-11;
 Matches 29; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

OY 2 HWSYGLRPGSGPSLQVKNKXFGITELSS---GPSLHWSYGLRP 45

Db 2 HWSYGLRPGSGPSLQVKNKXFGITELSS---GPSLHWSYGLRP 49

RESULT 6
 AAU11422
 ID AAU11422 standard; peptide; 28 AA.
 XX AC AAU11422;
 XX DT 12-MAR-2002 (first entry)
 XX DE Synthetic immunogen peptide 3.
 XX KW Gonadotropin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.

XX Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.

XX Key Location/Qualifiers
 FT Peptide 1..15
 FT /note= "Tetanus toxoid sequence (830-844 aa)"
 FT Peptide 16..19
 FT /note= "Spacer peptide"
 FT Peptide 20..28
 FT /note= "Gonadotropin releasing hormone epitope"
 FT Modified-site 29
 FT /note= "Amidated glycine or glycineamide"

XX WO200185763-A2.
 XX 15-NOV-2001.
 XX 04-MAY-2001; 2001WO-US014363.
 XX 05-MAY-2000; 2000US-0202328P.
 XX (APHT-) APHTON CORP.
 XX Grimes S, Michaeli D, Stevens VC;
 XX WPI; 2002-049440/06.
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.

XX Claim 11; Page 8; 43pp; English.

CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone (LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention

XX Sequence 28 AA;
 SQ

Query Match 55.7%; Score 136; DB 5; Length 28;
 Best Local Similarity 93.1%; Pred. No. 2.6e-10;

Matches 27; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 17 QYIKANSKFIGITELSSGFSLHWSYGLRP 45
 Db 1 QYIKANSKFIGITEL--GFSLHWSYGLRP 27

RESULT 7
 AAR62723
 XX AAR62723 standard; peptide; 47 AA.
 AC AAR62723;
 XX
 DT 25-MAR-2003 (revised)
 DT 17-SEP-1995 (first entry)
 XX
 DE LHRH-containing immunogenic peptide.
 XX
 KW Helper T cell epitope; universal immune stimulator; invasin; haptan;
 KW vaccine; LHRH; luteinising hormone releasing hormone; prostate;
 KW androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..16 "invasin domain"
 FT /note= "invasin domain"
 FT Domain 19..35
 FT /note= "tetanus toxin helper T cell epitope"
 FT Domain 38..47
 FT /note= "LHRH haptan"
 XX
 WO9425060-A1.
 XX
 PD 10-NOV-1994.
 XX
 XX 28-APR-1994; 94WO-US004832.
 XX
 PR 27-APR-1993; 93US-00057166.
 PR 14-APR-1994; 94US-00229275.
 XX
 PA (LADD/) LADD A E.
 PA (WANG/) WANG C Y.
 PA (ZAMB/) ZAMB T.
 XX
 PI Ladd AE, Wang CY, Zamb T;
 XX
 DR WPI; 1994-357910/44.
 XX
 PT Immunogenic luteinising hormone releasing hormone peptide(s) - that
 PT suppress LHRH activity in males and females.
 XX
 PS Claim 8; Page 88; 213pp; English.
 XX
 CC Synthetic immunogenic peptides are provided in which a universal immune
 CC stimulator is linked to a peptide or protein haptan containing B cell
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
 CC potent immune responses to the coupled peptide or protein. The stimulator
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
 CC immune response to the coupled peptide in members of a heterogeneous
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
 CC sequence from the invasin protein of Yersinia. Spacer amino acid
 CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
 CC domains and between the immune stimulator and haptan components. When the
 CC haptan is LHRH, then optionally the invasin domain can be omitted from
 CC the immune stimulator component. The present sequence represents an LHRH-
 CC containing immunogenic peptide as above which can be used as a potent
 CC vaccine for treating e.g. prostatic hyperplasia, androgen-dependent
 CC carcinoma, prostatic carcinoma, testicular carcinoma, endometriosis,
 CC benign uterine tumours, recurrent functional ovarian cysts, (severe)
 CC premenstrual syndrome or oestrogen-dependent breast cancer, or for
 CC induction of infertility. (Updated on 25-MAR-2003 to correct FN field.)
 XX

SQ Sequence 47 AA;
 Query Match 46.9%; Score 114.5; DB 2; Length 47;
 Best Local Similarity 72.7%; Pred. No. 2.8e-07;
 Matches 24; Conservative 0; Mismatches 6; Indels 3; Gaps 1;

QY 13 GPSLQYIKANSKFIGITELSSGFSLHWSYGLRP 45
 Db 17 GGGKQYIKANSKFIGITELGGE--HWSYGLRP 46

RESULT 8
 AAR62701
 ID AAR62701 standard; peptide; 27 AA.
 XX
 AC AAR62701;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-SEP-1995 (first entry)
 XX
 DE LHRH-containing immunogenic peptide.
 XX
 KW Helper T cell epitope; universal immune stimulator; invasin; haptan;
 KW vaccine; LHRH; luteinising hormone releasing hormone; prostate;
 KW androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Domain 1..17
 FT /note= "tetanus toxin helper T cell epitope"
 FT Domain 18..27
 FT /note= "LHRH haptan"
 XX
 WO9425060-A1.
 XX
 PD 10-NOV-1994.
 XX
 XX 28-APR-1994; 94WO-US004832.
 XX
 PR 27-APR-1993; 93US-00057166.
 PR 14-APR-1994; 94US-00229275.
 XX
 PA (LADD/) LADD A E.
 PA (WANG/) WANG C Y.
 PA (ZAMB/) ZAMB T.
 XX
 PI Ladd AE, Wang CY, Zamb T;
 XX
 DR WPI; 1994-357910/44.
 XX
 PT Immunogenic luteinising hormone releasing hormone peptide(s) - that
 PT suppress LHRH activity in males and females.
 XX
 PS Claim 8, 12; Page 84; 213pp; English.
 XX
 CC Synthetic immunogenic peptides are provided in which a universal immune
 CC stimulator is linked to a peptide or protein haptan containing B cell
 CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
 CC potent immune responses to the coupled peptide or protein. The stimulator
 CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
 CC immune response to the coupled peptide in members of a heterogeneous
 CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
 CC sequence from the invasin protein of Yersinia. Spacer amino acid
 CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
 CC domains and between the immune stimulator and haptan components. When the
 CC haptan is LHRH, then optionally the invasin domain can be omitted from
 CC the immune stimulator component. The present sequence represents an LHRH-
 CC containing immunogenic peptide as above which can be used
 CC as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-
 CC dependent carcinoma, prostatic carcinoma, testicular carcinoma,
 CC endometriosis, benign uterine tumours, recurrent functional ovarian
 CC cysts, (severe) premenstrual syndrome or oestrogen-dependent breast

KW Leukotoxin; gonadotropin-releasing hormone; GnRH; immunosterilisation;
 KW immunocontraception; vaccine; feline; canine; equine; cervine.
 XX
 OS Mannheimia haemolytica.
 OS Mammalia.
 OS Chimeric.
 XX
 PN WO9962545-A2.
 XX
 PD 09-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-CA000493.
 XX
 PR 04-JUN-1998; 98US-0088024P.
 PR 06-MAY-1999; 99US-00306689.
 XX
 XX (BIOS-) BIOTSTAR INC.
 PA
 PI Robbins SC;
 XX
 DR WPI; 2000-086857/07.
 DR N-PSDB; AAZ55700.
 XX
 XX Hormone immunogens, analogues or antibodies used to manufacture vaccines
 PT for suppression of reproductive behavior and fertility in vertebrates.
 PT
 PS Claim 20; Fig 6A-6F; 88pp; English.
 XX
 CC This sequence represents a fusion protein comprising gonadotropin-
 CC releasing hormone (GnRH) immunogens and a Pasteurella haemolytica
 CC leukotoxin (LKT) protein. The fusion protein comprises, in the N to C-
 CC terminal direction, a synthetic peptide sequence (AAV58364), an eight
 CC copy GnRH multimer (composed of two copies of the 4xGnRH multimer
 CC sequence of AAV58363), the LKT protein (which functions as a carrier
 CC protein), and a second eight copy GnRH multimer. The fusion protein may
 CC be used in a vaccine composition for prepubertal administration to a
 CC vertebrate subject to result in prolonged suppression of reproductive
 CC behaviour and/or fertility. GnRH immunogens, analogues or antibodies that
 CC cross-react with endogenous GnRH of a vertebrate subject are used to
 CC manufacture a composition or vaccine for immunosterilisation or
 CC immunocontraception of feline, canine, equine or cervine subjects. The
 CC vaccines are used to suppress reproductive behaviour and/or fertility for
 CC at least 10 months. The prepubertal administration results in a
 CC prolonged, long-term suppression of testicular development and/or
 CC function in males, or a prolonged, long-term suppression of ovarian
 CC development and/or function in females. The methods provide a viable and
 CC desirable alternative to surgical forms of sterilisation that are
 CC currently used. (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 695 AA;
 Query Match 44.5%; Score 108.5; DB 3; Length 695;
 Best Local Similarity 50.0%; Pred. No. 4.3e-05;
 Matches 22; Conservative 0; Mismatches 11; Indels 11; Gaps 1;
 QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGSLHWSYGLRP 45
 Db 36 HWSYGLRPGSGQDSY-----GLRPGSGQHSYGLRP 68
 RESULT 12
 ID AAY58133
 XX AAY58133 standard; protein; 695 AA.
 AC AAY58133;
 XX
 XX 12-SEP-2003 (revised)
 DT 07-MAR-2000 (first entry)
 XX
 XX Gonadotropin releasing hormone-leukotoxin fusion protein.
 DE
 DE Gonadotropin releasing hormone; GnRH; leukotoxin; LKT; fusion protein;
 KW antibody; immunogenic; chimeric; vaccine; testosterone; androgenic;
 KW

KW non-androgenic; steroid; reduction; weight gain; muscle distribution;
 KW fat distribution; male pattern; boar taint; flavour; impairment;
 KW reliable; immunocastration; meat production.
 XX
 OS Mannheimia haemolytica.
 OS Chimeric.
 XX
 PN WO9956771-A2.
 XX
 PD 11-NOV-1999.
 XX
 PF 05-MAY-1999; 99WO-CA000360.
 XX
 PR 05-MAY-1998; 98US-0084217P.
 XX
 XX (BIOS-) BIOTSTAR INC.
 PA
 PI Manns JG, Acres SD, Harland R;
 XX
 DR WPI; 2000-062125/05.
 DR N-PSDB; AA246400.
 XX
 XX Production of uncastrated male food animals using vaccines.
 PT
 PS Claim 22; Fig 3A-3F; 87pp; English.
 XX
 CC This sequence represents a chimeric gonadotropin releasing hormone (GnRH)
 CC -leukotoxin (LKT) fusion protein, which may be used as a vaccine. The LKT
 CC portion of the protein acts to enhance the immunogenicity of the
 CC multimeric GnRH portion (AAV58135). The invention relates to a method of
 CC using two GnRH immunogen vaccines to produce uncastrated male animals for
 CC meat production, one vaccination prior to or during the fattening period
 CC to reduce circulating testosterone levels, and the second vaccination
 CC about 2-8 weeks before slaughter to substantially reduce androgenic
 CC and/or non-androgenic steroids. The invention is used to produce food
 CC animals that exhibit the weight gain and muscle/fat distribution of male
 CC animals without the problems associated with male animals. Such problems
 CC include "boar taint", a urine-like odour found in cooked meat of
 CC uncastrated pigs which is caused by steroids stored in the tissues, and
 CC similar flavour impairments in the meat of other intact male animals. The
 CC invention is more reliable than prior art immunocastration techniques.
 CC (Updated on 12-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 695 AA;
 Query Match 44.5%; Score 108.5; DB 3; Length 695;
 Best Local Similarity 50.0%; Pred. No. 4.3e-05;
 Matches 22; Conservative 0; Mismatches 11; Indels 11; Gaps 1;
 QY 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSSGSLHWSYGLRP 45
 Db 36 HWSYGLRPGSGQDSY-----GLRPGSGQHSYGLRP 68
 RESULT 13
 ID AAW03944
 XX AAW03944 standard; protein; 49 AA.
 AC AAW03944;
 XX
 XX 20-NOV-1996 (first entry)
 DT
 XX GnRH 4-repeat sequence.
 DE
 DE Leukotoxin; LKT; gonadotropin-releasing hormone; GnRH; fusion protein;
 KW immunogen; vaccine; fertility control; contraceptive; sterilisation;
 KW PCB113; PCB111.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Peptide 1..10
 FT


```

FT Peptide /label= GnRH
FT 11..13 /label= Spacer
FT Peptide 14..23 /label= GnRH
FT Peptide 24..26 /label= Spacer
FT Peptide 27..36 /label= GnRH
FT Peptide 37..39 /label= Spacer
FT Peptide 40..49 /label= GnRH
XX
XX WO9624675-A1.
XX
XX 15-AUG-1996.
XX
XX 24-JAN-1996; 96WO-CA000049.
XX
XX 10-FEB-1995; 95US-00387156.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
XX
XX Potter AA, Manns JG;
XX
XX WPI: 1996-384447/38.
XX
XX N-PSDB; AAT37178.
XX
XX Gonadotropin-releasing hormone multimer fusion proteins - with leukotoxin
XX polypeptide for increased immunogenicity, useful in antifertility vaccine
XX prodn.
XX
XX Example 2; Fig 1B; 87pp; English.
XX
XX A synthetic DNA sequence (AAT37178) codes for a gonadotropin releasing
XX hormone (GnRH) tetramer (AAW03944), in which the 4 GnRH repeat units are
XX separated by spacers designed to increase immunogenicity. The DNA
XX sequence was incorporated into vector pAA352 (ATCC 68283), which contains
XX a truncated leukotoxin gene (LXT 352) derived from Pasteurella
XX haemolytica, to give plasmid pCB113 (AAT37176). Escherichia coli
XX transformants produce an LXT-GnRH fusion protein (see also AAW03942 and
XX AAW03943) useful as a vaccine for fertility control of domestic or farm
XX animals
XX
XX SQ Sequence 49 AA;
XX
XX Query Match 43.4%; Score 106; DB 2; Length 49;
XX Best Local Similarity 50.0%; Pred. No. 3.6e-06;
XX Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
XX
XX QY 2 HWSYGLRPGSGPSLQYIKANSKFGITELSSGSLHWSYGLRP 45
XX |||||
XX Db 2 HWSYGLRPGSGSQDWSY-----GLR--PGSSQHSYGLRP 35
XX
XX
XX RESULT 14
XX AAW79567
XX ID AAW79567 standard; protein; 49 AA.
XX
XX AC AAW79567;
XX
XX 24-DEC-1998 (first entry)
XX
XX GnRH-2.
XX
XX Gonadotropin releasing hormone; GnRH; decapeptide; hypothalamus; spacer;
XX LH; luteinising hormone; FSH; follicle stimulating hormone; vertebrate;
XX pyroglu; chimera; leukotoxin polypeptide; multimer; vaccine; tumour;
XX immunogenic.
XX
XX Synthetic.
XX
XX

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PN WO9806848-A1.
XX
XX 19-FEB-1998.
XX
XX 08-AUG-1997; 97WO-CA000359.
XX
XX 09-AUG-1996; 96US-00694865.
XX
XX (UYSA-) UNIV SASKATCHEWAN.
XX
XX Potter AA, Manns JG;
XX
XX WPI: 1998-159540/14.
XX
XX N-PSDB; AAV61529.
XX
XX Chimeric protein of leukotoxin and gonadotropin releasing hormone -
XX useful for, e.g. preparation of vaccines for reduction of incidence of
XX mammary tumours in mammals.
XX
XX Disclosure; Fig 1B; 118pp; English.
XX
XX The present sequence represents a recombinantly produced or chemically
XX synthesised Gonadotropin releasing hormone-2 (GnRH-2) polypeptide, which
XX contains four copies of the GnRH decapeptide (AAV61528) and triplet amino
XX acid spacers between each of these sequences. This decapeptide is
XX secreted naturally by the hypothalamus which controls release of both the
XX luteinising hormone (LH) and the follicle stimulating hormone (FSH) in
XX vertebrates. This sequence, as compared to the native peptide, has been
XX found to have an N-terminal Gln rather than a pyroglu residue, and also
XX contains substitutions at amino acid residues 15 and 41, whereby His is
XX replaced by Asp. This produces an alternating multimeric GnRH sequence
XX which is highly immunogenic that can be used in the construction of a
XX chimeric protein that comprises a leukotoxin polypeptide, several
XX multimers, and the GnRH sequence. The chimeric protein can be used as a
XX vaccine to help reduce the incidence of mammary tumours in a mammalian
XX individual
XX
XX SQ Sequence 49 AA;
XX
XX Query Match 43.4%; Score 106; DB 2; Length 49;
XX Best Local Similarity 50.0%; Pred. No. 3.6e-06;
XX Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;
XX
XX QY 2 HWSYGLRPGSGPSLQYIKANSKFGITELSSGSLHWSYGLRP 45
XX |||||
XX Db 2 HWSYGLRPGSGSQDWSY-----GLR--PGSSQHSYGLRP 35
XX
XX
XX RESULT 15
XX AAW61542
XX ID AAW61542 standard; protein; 49 AA.
XX
XX AC AAW61542;
XX
XX 27-OCT-1998 (first entry)
XX
XX Peptide hormone GnRH-2 decapeptide (4 copies) fragment.
XX
XX GnRH; gonadotropin releasing hormone peptide hormone; leukotoxin;
XX immunisation; endogenous molecule; vaccine; ear; immunogen; carrier;
XX immune response; hormone receptor; cancerous cell; domestic animal;
XX porcine; bovine; luteinizing hormone; follicle stimulating hormone;
XX immunocastrate.
XX
XX Synthetic.
XX
XX WO9834639-A1.
XX
XX 13-AUG-1998.
XX
XX 04-FEB-1998; 98WO-CA000059.
XX
XX 05-FEB-1997; 97US-0036883P.
XX

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XX (BIOS-) BIOSTAR INC.
XX
XX PI Harland R, Manns JG, Acres SD;
XX
XX WPI; 1998-448952/38.
XX DR N-PSDB; AAV45190.
XX
XX Immunisation against endogenous molecules by administering vaccine to ear
XX PT - useful to elicit efficient and uniform immune response against e.g.
XX PT gonadotrophin releasing hormone to immunocastrate pigs and cattle.
XX
XX PS Example 1; Fig 1B; 61pp; English.
XX
XX This represents the amino acid sequence of the gonadotrophin releasing
XX hormone (GnRH-2) decapeptide fragment used in the chimeric leukotoxin-
XX GnRH polypeptide gene fusions. This is used to exemplify the method of
XX invention of immunisation against endogenous molecules by administering a
XX vaccine which comprises an immunogen and a carrier to the ear of the
XX mammal. The method is useful for eliciting an efficient and uniform
XX immune response to block or suppress the activity of an endogenous
XX hormone, hormone receptor, agonist or antagonist in a vaccinated subject,
XX or to elicit an immune response against a targeted endogenous cell type
XX (e.g. a cancerous or otherwise diseased cell). It is especially useful to
XX reduce the levels of GnRH in domestic animals, especially in porcine or
XX bovine species. The use of GnRH immunogens in the vaccine reduces the
XX levels of luteinizing hormone and follicle stimulating hormone and helps
XX in immunocastrating the animal. Administration of vaccine compositions to
XX the ear instead of intramuscular administration into the neck increases
XX the efficiency of vaccination of mammals against endogenous immunogens,
XX and may increase uniformity of vaccine presentation since the ear is
XX relatively uniform from animal to animal
XX
XX SQ Sequence 49 AA;

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Query Match          43.4%; Score 106; DB 2; Length 49;
Best Local Similarity 50.0%; Pred. No. 3.6e-06;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

OY 2 HWSYGLRPGSSGSPSLQYIKANSKFGITELSSGSLHWSYGLRP 45
   . ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 HWSYGLRPGSSGSPSLQYIKANSKFGITELSSGSLHWSYGLRP 35
   . ||||| ||||| ||||| ||||| ||||| |||||

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Search completed: March 10, 2004, 09:12:14
Job time : 70.2685 secs

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OM protein - protein search, using sw model

Run on: March 10, 2004, 09:16:59 ; Search time 36.1556 Seconds
(without alignments)
268.645 Million cell updates/sec

Title: US-09-848-834A-19

Perfect score: 244

Sequence: 1 XHWSYGLRPGSSGSLQYK.....GITELSGPSLHWSYGLRXP 46

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 21153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	147.5	60.5	47	9	US-09-848-834A-17
5	145	59.4	50	9	US-09-848-834A-18
6	136	55.7	28	9	US-09-848-834A-11
7	113.5	46.5	27	14	US-10-076-674-7
8	113.5	46.5	27	15	US-10-355-161A-7
9	108.5	44.5	695	10	US-09-305-924-13
10	106	43.4	49	9	US-09-019-010-4
11	106	43.4	49	10	US-09-305-924-11
12	91	37.3	40	10	US-09-964-201A-35
13	91	37.3	41	10	US-09-964-201A-34
14	89	36.5	34	9	US-09-848-834A-13
15	89	36.5	36	9	US-09-848-834A-16

Sequence 26, Appl
Sequence 29, Appl
Sequence 30, Appl
Sequence 31, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 14, Appl
Sequence 8, Appl
Sequence 3, Appl
Sequence 15, Appl
Sequence 4, Appl
Sequence 46, Appl
Sequence 47, Appl
Sequence 2, Appl
Sequence 23, Appl
Sequence 23, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 9, Appl
Sequence 177, App
Sequence 143, App
Sequence 143, App
Sequence 147, App
Sequence 149, App
Sequence 141, App
Sequence 145, App
Sequence 1, Appl
Sequence 2, Appl
Sequence 4, Appl

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20 10 US-09-964-201A-29
20 10 US-09-964-201A-30
20 10 US-09-964-201A-31
37 9 US-09-848-834A-14
33 9 US-09-848-834A-12
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158 14 US-10-297-942-8
137 14 US-10-297-856-3
287 14 US-10-295-074-15
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16 9 US-09-848-834A-2
17 15 US-10-346-563-23
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887 14 US-10-241-596-147
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1315 14 US-10-241-596-141
1315 15 US-10-452-024-145
31 14 US-10-237-656-1
15 9 US-09-862-849-2
15 9 US-09-785-215-4

ALIGNMENTS

RESULT 1

US-09-848-834A-19
; Sequence 19, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 19
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human
; OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 830-844 of Tetan
; OTHER INFORMATION: toxoid precursor (Tentoxylisin) linked by a spacer to amino acic
; OTHER INFORMATION: sequence 1-10 of GnRH
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
; NAME/KEY: MOD RES
; LOCATION: (46)..(46)
; OTHER INFORMATION: Amidated glycine or glycylamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
; NAME/KEY: PEPTIDE
; LOCATION: (11)..(16)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(31)
; OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor

OTHER INFORMATION: (Tentoxylisin)
NAME/KEY: PEPTIDE
LOCATION: (32)..(37)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (38)..(46)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-19

Query Match 99.2%; Score 242; DB 9; Length 46;
Best Local Similarity 100.0%; Pred. No. 2.4e-23;
Matches 44; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGSLQYIKANSKFIGITELSSGSPSLHWSYGLRP 45
DB 2 HWSYGLRPGSSGSLQYIKANSKFIGITELSSGSPSLHWSYGLRP 45

RESULT 2

US-09-848-834A-15
Sequence 15, Application US/09848834A
Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Apton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.0

SEQ ID NO 15

LENGTH: 31

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the Gn

OTHER INFORMATION: RH hormone linked by a spacer to amino sequence 830-844 of the Te

OTHER INFORMATION: tanus toxoid precursor (Tentoxylisin)

NAME/KEY: MOD_RES

LOCATION: (1)..(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: PEPTIDE

LOCATION: (1)..(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE

LOCATION: (11)..(16)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (17)..(31)

OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxoid precursor

OTHER INFORMATION: (Tentoxylisin)

US-09-848-834A-15

Query Match 66.0%; Score 161; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 2.5e-13;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGSLQYIKANSKFIGITEL 31
DB 2 HWSYGLRPGSSGSLQYIKANSKFIGITEL 31

RESULT 3

US-09-848-834A-20

Sequence 20, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Apton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 51
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human

OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 378-398 of Plasmic

OTHER INFORMATION: ium falciparum circumsporozoite (CSP) protein

NAME/KEY: MOD_RES

LOCATION: (1)..(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: MOD_RES

LOCATION: (51)..(51)

OTHER INFORMATION: Amidated glycine or glycylamide

NAME/KEY: PEPTIDE

LOCATION: (1)..(10)

OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE

LOCATION: (11)..(16)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (17)..(36)

OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum

OTHER INFORMATION: circumsporozoite (CSP) protein

NAME/KEY: PEPTIDE

LOCATION: (37)..(42)

OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE

LOCATION: (43)..(51)

OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-20

Query Match 65.8%; Score 160.5; DB 9; Length 51;

Best Local Similarity 66.0%; Pred. No. 5e-13;

Matches 33; Conservative 3; Mismatches 7; Indels 7; Gaps 2;

QY 2 HWSYGLRPGSSGSL-----QYIKANSKFIGITELSSGSPSLHWSYGLRP 45
DB 2 HWSYGLRPGSSGSLDEKKIAKMKASSVF-NVWNSGSPSLHWSYGLRP 50

RESULT 4

US-09-848-834A-17

Sequence 17, Application US/09848834A

Patent No. US20020076416A1

GENERAL INFORMATION:

APPLICANT: Apton Corporation

TITLE OF INVENTION: Chimeric Peptide Immunogens

FILE REFERENCE: 1102865-0047

CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04

PRIOR APPLICATION NUMBER: 60/202,328

PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PatentIn version 3.0

SEQ ID NO 17

LENGTH: 47

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the (

OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of

OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid seq

OTHER INFORMATION: uence 2-10 of the GnRH hormone

NAME/KEY: MOD_RES

LOCATION: (1)..(1)

OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: MOD_RES

LOCATION: (47)..(47)
OTHER INFORMATION: Amidated-glycine or glycylamide
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KEY: PEPTIDE
LOCATION: (11)..(18)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (19)..(34)
OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein,
NAME/KEY: PEPTIDE
LOCATION: (35)..(38)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (39)..(47)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-17
Query Match 60.5%; Score 147.5; DB 9; Length 47;
Best Local Similarity 62.5%; Pred. No. 2e-11; 7; Indels 7; Gaps 2;
Matches 30; Conservative 4; Mismatches 7
QY 2 HWSYGLRPGSSGSPSLQYKANSKFTIGI----TELSSGSPSLHWSYGLRP 45
|||||
DB 2 HWSYGLRPGSSGSPSLKLL--SEIKGVIVHRLEGVGGPSLHWSYGLRP 46
|||||
RESULT 5
US-09-848-834A-18
; Sequence 18, Application US/09848834A
; Patent No. US20020076416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 18
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human
; OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 947-967 of the Tet
; OTHER INFORMATION: anus toxoid precursor (Tentoxylisin) protein linked by a spacer t
; OTHER INFORMATION: o amino acid sequence 2-10 of human GnRH
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD RES
LOCATION: (30)..(50)
OTHER INFORMATION: Amidated glycine or glycylamide
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KEY: PEPTIDE
LOCATION: (11)..(16)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (17)..(37)
OTHER INFORMATION: Amino acid sequence 947-967 of the Tetanus toxoid precursor (Tent
OTHER INFORMATION: oxylysin
NAME/KEY: PEPTIDE
LOCATION: (38)..(41)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (42)..(50)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone

US-09-848-834A-18
Query Match 59.4%; Score 145; DB 9; Length 50;
Best Local Similarity 60.4%; Pred. No. 4.4e-11;
Matches 29; Conservative 6; Mismatches 9; Indels 4; Gaps 1;
QY 2 HWSYGLRPGSSGSPSLQYKANSKFTIGITELSS----GPSLHWSYGLRP 45
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DB 2 HWSYGLRPGSSGSPSLFNNFTVSFLRVKPKVSASHLEGPSLHWSYGLRP 49
|||||
RESULT 6
US-09-848-834A-11
; Sequence 11, Application US/09848834A
; Patent No. US20020076418A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 830-844 of tl
; OTHER INFORMATION: Tetanus toxoid precursor (Tentoxylisin) linked by a spacer to a
; OTHER INFORMATION: ino acid sequence 2-10 of the GnRH hormone
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: Amidated-glutamine
NAME/KEY: MOD RES
LOCATION: (28)..(28)
OTHER INFORMATION: Amidated-glycine or glycylamide
NAME/KEY: PEPTIDE
LOCATION: (1)..(15)
OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus Toxoid Precursor
; OTHER INFORMATION: (Tentoxylisin)
NAME/KEY: PEPTIDE
LOCATION: (16)..(19)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (20)..(28)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-11
Query Match 55.7%; Score 136; DB 9; Length 28;
Best Local Similarity 93.1%; Pred. No. 3.1e-10;
Matches 27; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
QY 17 QYKANSKFTIGITELSSGSPSLHWSYGLRP 45
|||||
DB 1 QYKANSKFTIGITEL--GPSLHWSYGLRP 27
|||||
RESULT 7
US-10-076-674-7
; Sequence 7, Application US/10076674
; Publication No. US20030165478A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/076,674
; CURRENT FILING DATE: 2002-04-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7

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; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human
US-10-076-674-7

Query Match 46.5%; Score 113.5; DB 14; Length 27;
Best Local Similarity 79.3%; Pred. No. 2e-07;
Matches 23; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 17 QYIKANSKFITELSSGSPSLHWSYGLRP 45
Db 3 QYIKANSKFITELSSGSPSLHWSYGLRP 26

RESULT 8
US-10-355-161A-7
; Sequence 7, Application US/10355161A
; Publication No. US2004009897A1
; GENERAL INFORMATION:
; APPLICANT: Sokoll, Kenneth K.
; TITLE OF INVENTION: Stabilized Synthetic Immunogen Delivery System
; FILE REFERENCE: Immunogen Delivery System
; CURRENT APPLICATION NUMBER: US/10/355,161A
; CURRENT FILING DATE: 2003-01-31
; PRIOR APPLICATION NUMBER: US 10/076674
; PRIOR FILING DATE: 2002-02-14
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 7
; LENGTH: 27
; TYPE: PRT
; ORGANISM: Human
US-10-355-161A-7

Query Match 46.5%; Score 113.5; DB 15; Length 27;
Best Local Similarity 79.3%; Pred. No. 2e-07;
Matches 23; Conservative 0; Mismatches 1; Indels 5; Gaps 1;

Qy 17 QYIKANSKFITELSSGSPSLHWSYGLRP 45
Db 3 QYIKANSKFITELSSGSPSLHWSYGLRP 26

RESULT 9
US-09-305-924-13
; Sequence 13, Application US/09305924A
; Publication No. US20030091579A1
; GENERAL INFORMATION:
; APPLICANT: Jack G. Manns
; APPLICANT: Stephen D. Acres
; APPLICANT: Richard Harland
; TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION
; FILE REFERENCE: 9001-0048
; CURRENT APPLICATION NUMBER: US/09/305,924A
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,217
; EARLIER FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 13
; LENGTH: 695
; TYPE: PRT
; ORGANISM: GRH
US-09-305-924-13

Query Match 44.5%; Score 108.5; DB 10; Length 695;
Best Local Similarity 50.0%; Pred. No. 3.3e-05;
Matches 22; Conservative 0; Mismatches 11; Indels 11; Gaps 1;

Qy 2 HWSYGLRPGSGPSLOYIKANSKFITELSSGSPSLHWSYGLRP 45
Db 36 HWSYGLRPGSGSQDWSY-----GLRPGSGSHWSYGLRP 68

RESULT 10
US-09-019-010-4
; Sequence 4, Application US/09019010
; Patent No. US20010014330A1
; GENERAL INFORMATION:
; APPLICANT: HARLAND, RICHARD
; APPLICANT: MANN, JOHN G.
; APPLICANT: ACRES, STEPHEN D.
; TITLE OF INVENTION: IMMUNIZATION AGAINST ENDOGENOUS
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROBINS & ASSOCIATES
; STREET: 90 MIDDLEFIELD ROAD, SUITE 200
; CITY: MENLO PARK
; STATE: CA
; COUNTRY: USA
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/019,010
; FILING DATE: 05-FEB-1998
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/036,883
; FILING DATE: 05-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: MCCracken, Thomas P.
; REGISTRATION NUMBER: 38,548
; REFERENCE/DOCKET NUMBER: 9001-0035
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 325-7812
; TELEFAX: (650) 325-7823
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 49 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-019-010-4

Query Match 43.4%; Score 106; DB 9; Length 49;
Best Local Similarity 50.0%; Pred. No. 3.5e-06;
Matches 22; Conservative 1; Mismatches 11; Indels 10; Gaps 2;

Qy 2 HWSYGLRPGSGPSLOYIKANSKFITELSSGSPSLHWSYGLRP 45
Db 2 HWSYGLRPGSGSQDWSY-----GLRPGSGSHWSYGLRP 35

RESULT 11
US-09-305-924-11
; Sequence 11, Application US/09305924A
; Publication No. US20030091579A1
; GENERAL INFORMATION:
; APPLICANT: Jack G. Manns
; APPLICANT: Stephen D. Acres
; APPLICANT: Richard Harland
; TITLE OF INVENTION: METHODS OF RAISING ANIMALS FOR MEAT PRODUCTION
; FILE REFERENCE: 9001-0048
; CURRENT APPLICATION NUMBER: US/09/305,924A
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,217
; EARLIER FILING DATE: 1998-05-05
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 11
; LENGTH: 49
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; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
; NAME/KEY: PEPTIDE
; LOCATION: (11)..(16)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(36)
; OTHER INFORMATION: Amino acid sequence 378-398 of the Malaria
; OTHER INFORMATION: (Plasmodium falciparum) circumsporozoite
; OTHER INFORMATION: (CSP) protein
US-09-848-834A-16

Query Match      36.5%; Score 89; DB 9; Length 36;
Best Local Similarity 63.3%; Pred. No. 0.00034;
Matches 19; Conservative 2; Mismatches 3; Indels 6; Gaps 1;

QY      2 HWSYGLRPGSSGPSL-----QYIKANSKF 25
      |||||
Db      2 HWSYGLRPGSSGPSLDEKKIAMEKASSVF 31
      |||||

Search completed: March 10, 2004, 10:25:50
Job time : 37.1556 secs
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 18.1965 Seconds
(without alignments)
133.345 Million cell updates/sec

Title: US-09-848-834A-17
Perfect score: 248
Sequence: 1 XHWSYGURPGSGPSLKLIS.....HRLEGVEGPSLHWSYGLRPX 47

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	
1	117	47.2	42	1	US-08-446-692-20	Sequence 20,	Appl
2	117	47.2	42	2	US-08-488-351A-20	Sequence 20,	Appl
3	116	46.8	27	1	US-08-446-692-19	Sequence 19,	Appl
4	116	46.8	27	2	US-08-488-351A-19	Sequence 19,	Appl
5	116	46.8	27	3	US-09-100-414B-36	Sequence 36,	Appl
6	116	46.8	27	4	US-09-303-323-36	Sequence 36,	Appl
7	116	46.8	27	4	US-09-770-014-36	Sequence 36,	Appl
8	116	46.8	45	1	US-08-446-692-33	Sequence 33,	Appl
9	116	46.8	45	2	US-08-488-351A-33	Sequence 33,	Appl
10	113	45.6	27	3	US-09-100-414B-43	Sequence 43,	Appl
11	113	45.6	27	3	US-09-303-323-43	Sequence 43,	Appl
12	113	45.6	27	4	US-09-770-014-43	Sequence 43,	Appl
13	110	44.4	31	3	US-09-100-414B-55	Sequence 55,	Appl
14	110	44.4	31	3	US-09-303-323-55	Sequence 55,	Appl
15	110	44.4	31	4	US-09-770-014-55	Sequence 55,	Appl
16	108	43.5	27	3	US-09-100-414B-41	Sequence 41,	Appl
17	108	43.5	27	3	US-09-100-414B-47	Sequence 47,	Appl
18	108	43.5	27	3	US-09-303-323-41	Sequence 41,	Appl
19	108	43.5	27	3	US-09-303-323-47	Sequence 47,	Appl
20	108	43.5	27	4	US-09-770-014-41	Sequence 41,	Appl
21	108	43.5	27	4	US-09-770-014-47	Sequence 47,	Appl
22	108	43.5	45	3	US-09-100-414B-45	Sequence 45,	Appl
23	108	43.5	45	3	US-09-303-323-45	Sequence 45,	Appl
24	108	43.5	45	4	US-09-770-014-45	Sequence 45,	Appl
25	107	43.1	31	3	US-09-100-414B-59	Sequence 59,	Appl
26	107	43.1	31	3	US-09-303-323-59	Sequence 59,	Appl
27	107	43.1	31	4	US-09-770-014-59	Sequence 59,	Appl

28	106	42.7	28	3	US-09-100-414B-38	Sequence 38,	Appl
29	106	42.7	28	3	US-09-303-323-38	Sequence 38,	Appl
30	106	42.7	28	4	US-09-770-014-38	Sequence 38,	Appl
31	106	42.7	40	2	US-08-460-503-10	Sequence 10,	Appl
32	106	42.7	40	4	US-09-148-711A-10	Sequence 10,	Appl
33	105	42.3	31	3	US-09-100-414B-53	Sequence 53,	Appl
34	105	42.3	31	3	US-09-303-323-53	Sequence 53,	Appl
35	105	42.3	31	4	US-09-770-014-53	Sequence 53,	Appl
36	105	42.3	47	3	US-09-100-414B-60	Sequence 60,	Appl
37	105	42.3	47	3	US-09-303-323-60	Sequence 60,	Appl
38	105	42.3	47	4	US-09-770-014-60	Sequence 60,	Appl
39	105	42.3	49	3	US-09-100-414B-57	Sequence 57,	Appl
40	105	42.3	49	3	US-09-303-323-57	Sequence 57,	Appl
41	105	42.3	49	4	US-09-770-014-57	Sequence 57,	Appl
42	103.5	41.7	25	1	US-08-446-693-17	Sequence 17,	Appl
43	103.5	41.7	25	2	US-08-488-351A-17	Sequence 17,	Appl
44	103	41.5	27	3	US-09-100-414B-50	Sequence 50,	Appl
45	103	41.5	27	3	US-09-303-323-50	Sequence 50,	Appl

ALIGNMENTS

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RESULT 1
US-08-446-692-20
; Sequence 20, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0. Version #1.25

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SOFTWARE: PatentIn Release #1.0, Velsiol W1.1J
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 42 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PS-08-446-692-20

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Query Match      47.2% ; Score 117; DB 1; Length 42;
Best Local Similarity 82.8% ; Pred. No. 9.5e-09;
Matches 24; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Cy 18 LLSEIKGVIVHRLEGVEGFSLHWSYGLRP 46
      :|||:|||||:|||||:|||||:|||||:
Db 15 VI-SF-KGVIVHRLEGVGGE--HWSYGLRP 41

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QY 18 LLSEIKGVIVHRLEGVGSPSLHWSYGLRP 46
:|||||:|||||
pb 15 VLSEIKGVIVHRLEGVGGE--HWSYGLRP 41

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RESULT 2
US-08-488-351A-20
; Sequence 20, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,275
; FILING DATE: 14-APR-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/057,166
; FILING DATE: 27-APR-1992
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TYPE: amino acid
; LENGTH: 42 amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-488-351A-20

Query Match 47.2%; Score 117; DB 2; Length 42;
Best Local Similarity 82.8%; Pred. No. 9.5e-09;
Matches 24; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 18 LSEIKGVIVHRLGVGSPSLHWSYGLRP 45
;
Db 15 VLSEIKGVIVHRLGVGSGE--HWSYGLRP 41
;
RESULT 3
US-08-446-692-19
; Sequence 19, Application US/08446692
; Patent No. 5759551
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
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; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria C.H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4146 US2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)415-8745
; TELEFAX: (516)751-6849
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-446-692-19

Query Match 46.8%; Score 116; DB 1; Length 27;
Best Local Similarity 85.7%; Pred. No. 7.5e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVHRLGVGSPSLHWSYGLRP 46
;
Db 1 LSEIKGVIVHRLGVGSGE--HWSYGLRP 26
;
RESULT 4
US-08-488-351A-19
; Sequence 19, Application US/08488351A
; Patent No. 5843446
; GENERAL INFORMATION:
; APPLICANT: Ladd, Anna
; APPLICANT: Wang, Chang Yi
; APPLICANT: Zamb, Timothy
; TITLE OF INVENTION: Immunogenic LHRH peptide constructs
; TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Maria C.H. Lin
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: US
; ZIP: 10154-0053
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,351A
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/446,692
; FILING DATE: 7-JUN-1995
; CLASSIFICATION: 424
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;; PRIOR APPLICATION DATA: US 08/229,275
;; APPLICATION NUMBER: US 08/229,275
;; FILING DATE: 14-APR-1994
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/057,166
;; FILING DATE: 27-APR-1992
;; CLASSIFICATION: 424
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Maria C.H. Lin
;; REGISTRATION NUMBER: 29,323
;; REFERENCE/DOCKET NUMBER: 1151-4146 US2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212)415-8745
;; TELEFAX: (516)751-6849
;; INFORMATION FOR SEQ ID NO: 19:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-488-351A-19

Query Match 46.8%; Score 116; DB 2; Length 27;
Best Local Similarity 85.7%; Pred. No. 7.5e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHRLEGVEGSPSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26

RESULT 5
US-09-100-414B-36
; Sequence 36, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-100-414B-36

Query Match 46.8%; Score 116; DB 3; Length 27;

Best Local Similarity 85.7%; Pred. No. 7.5e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHRLEGVEGSPSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26

RESULT 6
US-09-303-323-36
; Sequence 36, Application US/09303323
; Patent No. 6228987
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 36:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-36

Query Match 46.8%; Score 116; DB 3; Length 27;
Best Local Similarity 85.7%; Pred. No. 7.5e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Qy 19 LSEIKGVIVHRLEGVEGSPSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26

RESULT 7
US-09-770-014-36
; Sequence 36, Application US/09770014
; Patent No. 6559282
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York

```
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
SOFTWARE: Word 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/770,014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/100,414
FILING DATE: 20-JUNE-1998
ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4157
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-770-014-36

Query Match 46.8%; Score 116; DB 4; Length 27;
Best Local Similarity 85.7%; Pred. No. 7.5e-09;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Oy 19 LSEIKGVIVHRLEGVGPSSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGPSSLHWSYGLRP 26

RESULT 8
US-08-446-692-33
Sequence 33, Application US/08446692
Patent No. 5759551
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-692-33

Query Match 46.8%; Score 116; DB 2; Length 45;
Best Local Similarity 85.7%; Pred. No. 1.4e-08;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

Oy 19 LSEIKGVIVHRLEGVGPSSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGPSSLHWSYGLRP 44

RESULT 9
US-08-488-351A-33
Sequence 33, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: US
ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 45 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-351A-33

Query Match 46.8%; Score 116; DB 2; Length 45;
Best Local Similarity 85.7%; Pred. No. 1.4e-08;
Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
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Matches 24; Conservative 0; Mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVHRLEGVEGSLHWSYGLRP 46
Db 19 LSEIKGVIVHRLEGVGGE--HWSYGLRP 44

RESULT 10

US-09-100-414B-43

; Sequence 43, Application US/09100414B

; Patent No. 6025468

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: NOVEL LHRH PEPTIDE

; TITLE OF INVENTION: IMMUNOGENS

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/100,414B

; FILING DATE: 20-JUNE-1998

; CLASSIFICATION: 424

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 27 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; US-09-100-414B-43

Query Match 45.6%; Score 113; DB 3; Length 27;

Best Local Similarity 82.1%; Pred. No. 1.9e-08;

Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVHRLEGVEGSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26

RESULT 11

US-09-303-323-43

; Sequence 43, Application US/09303323

; Patent No. 6228987

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: NOVEL LHRH PEPTIDE

; TITLE OF INVENTION: IMMUNOGENS

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/303,323
; FILING DATE: 30-APR-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-303-323-43

Query Match 45.6%; Score 113; DB 3; Length 27;

Best Local Similarity 82.1%; Pred. No. 1.9e-08;

Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVHRLEGVEGSLHWSYGLRP 46
Db 1 LSEIKGVIVHRLEGVGGE--HWSYGLRP 26

RESULT 12

US-09-770-014-43

; Sequence 43, Application US/09770014

; Patent No. 6559282

; GENERAL INFORMATION:

; APPLICANT: Wang, Chang Yi

; TITLE OF INVENTION: NOVEL LHRH PEPTIDE

; TITLE OF INVENTION: IMMUNOGENS

; NUMBER OF SEQUENCES: 106

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Morgan & Finnegan, L.L.P.

; STREET: 345 Park Avenue

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10154-0054

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC Windows

; SOFTWARE: Word 97

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/770,014

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/100,414

; FILING DATE: 20-JUNE-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Maria H. Lin

; REGISTRATION NUMBER: 29,323

; REFERENCE/DOCKET NUMBER: 1151-4157

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 212-758-4800

; TELEFAX: 212-751-6849

; INFORMATION FOR SEQ ID NO: 43:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 27 amino acids

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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-770-014-43

Query Match
Best Local Similarity 45.6%; Score 113; DB 4; Length 27;
Matches 23; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 19 LSEIKGVIVHRLGVGPGSLHWSYGLRP 46
Db 1 LSEIKGVIVHKLGVGGE--HWSYGLRP 26

RESULT 13
US-09-100-414B-55
; Sequence 55, Application US/09100414B
; Patent No. 6025468
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/100,414B
; FILING DATE: 20-JUNE-1998
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-303-323-55

Query Match
Best Local Similarity 44.4%; Score 110; DB 3; Length 31;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 19 LSEIKGVIVHRLGVGPGSLHWSYGLRP 46
Db 3 LSEIKGVIVHKLGVGGEHWSYGLRP 30

RESULT 15
US-09-770-014-55
; Sequence 55, Application US/09770014
; Patent No. 6859282
; GENERAL INFORMATION:
; APPLICANT: Wang, Chang Yi
; TITLE OF INVENTION: NOVEL LHRH PEPTIDE
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan & Finnegan, L.L.P.
; STREET: 345 Park Avenue
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10154-0054
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC Windows
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/770,014
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/100,414
; FILING DATE: 20-JUNE-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Maria H. Lin
; REGISTRATION NUMBER: 29,323
```

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; REFERENCE/DOCKET NUMBER: 1151-4157
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-758-4800
; TELEFAX: 212-751-6849
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-770-014-55

Query Match      44.4%; Score 110; DB 4; Length 31;
Best Local Similarity 78.6%; Pred. No. 5.6e-08;
Matches 22; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy      19 LSEIKGVIVHLEGVGEPGLHWSYGLRP 46
      |||||:|||||:|||||
Db      3 LSEIKGVIVHKLKGLVFGGEHWSYGLRP 30

Search completed: March 10, 2004, 09:28:56
Job time : 18.1965 secs
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 15.5642 Seconds
(without alignments)
309.015 Million cell updates/sec

Title: US-09-848-834A-18
Perfect score: 274
Sequence: 1 XHWSYGLRPGSGPSLFNFF.....VSASHLEGPSLHWSYGLRPX 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 78: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	114	41.6	1315	1 BTCLTN	tentoxilysin (EC 3
2	67	24.5	1297	2 S39791	neurotoxin - Clost
3	65	23.7	1286	1 BTCLAB	bontoxilysin (EC 3
4	64	23.4	1268	2 S33411	botulinum neurotox
5	64	23.4	1291	2 I40631	non-proteolytic bo
6	63	23.0	369	2 S48109	neurotoxin type F
7	63	23.0	1274	2 I40813	neurotoxin type F
8	63	23.0	1251	1 A48940	bontoxilysin (EC 3
9	62.5	22.8	1291	2 S46431	botulinum neurotox
10	62.5	22.8	1291	2 A49777	botulinum neurotox
11	62	22.6	1296	2 I40645	botulinum neurotox
12	61.5	22.4	91	2 JCR793	medaka-type gonado
13	61.5	22.4	92	1 RHRTG	gonadoliberin prec
14	61	22.3	366	2 S48110	neurotoxin type F
15	61	22.3	502	2 T36589	probable transmemb
16	59.5	21.7	1285	2 S70582	botulinum neurotox
17	59.5	21.7	1999	2 AB2018	hypothetical prote
18	59	21.5	67	2 I78541	gonadoliberin prec
19	59	21.5	92	1 RHVPG	gonadoliberin - pi
20	58	21.2	10	1 RHVPG	gonadoliberin - pi
21	58	21.2	10	1 RHSHG	gonadoliberin - sh
22	58	21.2	89	2 I51423	gonadoliberin prec
23	58	21.2	90	1 RHMSG	gonadoliberin prec
24	57.5	21.0	352	1 JVV524	coat protein VP2 -
25	57.5	21.0	836	2 JF0248	ATP-binding cass
26	57	20.8	665	2 H83403	hypothetical prote
27	56.5	20.6	98	2 I50739	gonadotropin-relea
28	56.5	20.6	345	2 A58519	hypothetical 345 p
29	56.5	20.6	367	2 S48106	neurotoxin type E

30	56.5	20.6	444	2	T24077	hypothetical prote
31	56.5	20.6	551	2	AC3572	lysine-tRNA ligase
32	56.5	20.6	658	2	S06744	staphylococcalase
33	56.5	20.6	1251	2	JH0256	botulinum neurotox
34	56.5	20.6	1252	2	S21178	botulinum neurotox
35	56	20.4	92	2	I50644	gonadoliberin I pr
36	56	20.4	141	2	S48593	probable methionyl
37	56	20.4	812	2	T01618	hypothetical prote
38	55.5	20.3	549	1	A47468	cytochrome-c oxida
39	55.5	20.3	658	2	A89786	staphylococcalase
40	55.5	20.3	715	2	A41511	staphylococcalase
41	55	20.1	496	2	T38197	probable myb-like
42	54.5	19.9	464	1	MNVUWC	nonstructural prot
43	54.5	19.9	3122	2	T17202	DNA-directed DNA p
44	54.5	19.9	5232	2	A45086	HC-toxin synthetas
45	54	19.7	10	1	RHAQ1	gonadoliberin I -

ALIGNMENTS

RESULT 1

BTCLTN
tentoxilysin (EC 3.4.24.68) precursor - Clostridium tetani
N/Alternate names: tetanus neurotoxin
C/Species: Clostridium tetani
C/Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 03-Jun-2002
C/Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364
R/Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U.; Hudel, EMBL J. 5, 2495-2502, 1986
A/Title: Tetanus toxin: Primary structure, expression in E. coli, and homology with b
A/Reference number: A25689; MUID:87053814; PMID:3536478
A/Accession: A25689
A/Molecule type: DNA
A/Residues: 1-1315 <BIS>
A/Cross-references: GB:X04436; NID:G40769; PIDN:CAA28033.1; PID:G40770
R/Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A/Title: The complete nucleotide sequence of tetanus toxin.
A/Reference number: A25757; MUID:87040747; PMID:3774547
A/Accession: A25757
A/Molecule type: DNA
A/Residues: 1-1315 <FAI>
A/Cross-references: GB:X06214; NID:G40773; PIDN:CAA29564.1; PID:G40774
A/Experimental source: strain CN3911
R/Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986
A/Title: Cloning, nucleotide sequencing, and expression of tetanus toxin fragment C in
A/Reference number: A25194; MUID:86085672; PMID:3510187
A/Accession: A25194
A/Molecule type: DNA
A/Residues: 743-1315 <FA2>
A/Cross-references: GB:W12739; NID:G144920; PIDN:AAA23282.1; PID:G144921
A/Accession: B25194
A/Molecule type: protein
A/Residues: 865-894 <FA3>
R/Matsuda, M.; Lei, D.L.; Sugimoto, N.; Ozutsumi, K.; Okabe, T.
Infect. Immun. 57, 3588-3593, 1989
A/Title: Isolation, purification, and characterization of fragment B, the NH-2-termina
A/Reference number: A60759; MUID:90035436; PMID:2478476
A/Accession: A60759
A/Molecule type: protein
R/Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, G.
J. Immunol. 142, 394-402, 1989
A/Title: Delination of several DB-restricted tetanus toxin T cell epitopes.
A/Reference number: JS0098; MUID:89039918; PMID:2463305
A/Contents: annotation; epitope region
R/Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, I.
Nature 359, 832-835, 1992
A/Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteol
A/Reference number: S27125; MUID:93063293; PMID:1331807
A/Contents: annotation

F:231/Active site: Glu #status predicted

Query Match 23.4%; Score 64; DB 2; Length 1291;
Best Local Similarity 62.5%; Pred. NO. 9.9;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SLFNNFTVSFWLRVPK 30
|.:|.:|.:|.:|.:|.:|
DB 921 SMFLDFSVSWIRIPK 936
|.:.|.:.|.:.|.:.|.:

RESULT 6
S48109
neurotoxin type F - Clostridium botulinum (fragment)
C:Species: Clostridium botulinum
C>Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Jul-1999
C:Accession: S48109
R:Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A:Title: Gene probes for identification of the botulin neurotoxin gene and specific residues
A:Reference number: S48103; MUID:94013372; PMID:8408542
A:Accession: S48109
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-369 <CAM>
A:Cross-references: EMBL:X70820; NID:g407790; PIDN:CAA50151.1; PID:g407791
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
C:Superfamily: tetanus toxin

Query Match 23.0%; Score 63; DB 2; Length 369;
Best Local Similarity 56.2%; Pred. NO. 3.2;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 15 SLFNNFTVSFWLRVPK 30
|.:|.:|.:|.:|.:|.:|
DB 295 SRQNFSISFWIRIPK 310
|.:.|.:.|.:.|.:.|.:

RESULT 7
I40813
neurotoxin type F - Clostridium botulinum
C:Species: Clostridium botulinum
C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999
C:Accession: I40813; S48108
R:East, A.K.; Richardson, P.T.; Allaway, D.; Collins, M.D.; Roberts, T.A.; Thompson, D.
FEMS Microbiol. Lett. 96, 225-230, 1992
A:Title: Sequence of the gene encoding type F neurotoxin of Clostridium botulinum.
A:Reference number: I40644
A:Accession: I40813
A>Status: preliminary; translated from GB/EMBL/DDEU
A:Molecule type: DNA
A:Residues: 1-1274 <RES>
A:Cross-references: GB:M92906; NID:g144866; PIDN:AAA3263.1; PID:g144867
R:Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A:Title: Gene probes for identification of the botulin neurotoxin gene and specific residues
A:Reference number: S48103; MUID:94013372; PMID:8408542
A:Accession: S48108
A>Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 634-1002 <CAM>
A:Cross-references: EMBL:X70816; NID:g407788; PIDN:CAA50147.1; PID:g407789
C:Superfamily: tetanus toxin
C:Keywords: neurotoxin

Query Match 23.0%; Score 63; DB 2; Length 1274;
Best Local Similarity 56.2%; Pred. NO. 13;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 15 SLFNNFTVSFWLRVPK 30
|.:|.:|.:|.:|.:|.:|
DB 928 SRQNFSISFWIRIPK 943
|.:.|.:.|.:.|.:.|.:

F:231/Active site: Glu #status predicted

Query Match 23.4%; Score 64; DB 2; Length 1268;
Best Local Similarity 62.5%; Pred. NO. 9.7;
Matches 10; Conservative 4; Mismatches 0; Gaps 0;

QY 15 SLFNNFTVSFWLRVPK 30
|.:|.:|.:|.:|.:|.:|
DB 920 SRQNFSISFWIRIPK 935
|.:.|.:.|.:.|.:.|.:

RESULT 5
I40631
non-proteolytic botulinum neurotoxin type B precursor - Clostridium botulinum
C:Species: Clostridium botulinum
C>Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
C:Accession: I40631; S48103; S48104; S36015
R:Hutson, R.A.; Collins, M.D.; East, A.K.; Thompson, D.E.
Curr. Microbiol. 28, 101-110, 1994
A:Title: Nucleotide sequence of the gene coding for non-proteolytic Clostridium botulinum
A:Reference number: I40631; MUID:94122659; PMID:7764370
A:Accession: I40631
A>Status: preliminary; translated from GB/EMBL/DDEU
A:Molecule type: DNA
A:Residues: 1-1291 <RES>
A:Cross-references: EMBL:X71343; NID:g296148; PIDN:CAA50482.1; PID:g296149
R:Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A:Title: Gene probes for identification of the botulin neurotoxin gene and specific id
A:Reference number: S48103; MUID:94013372; PMID:8408542
A:Accession: S48103
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 634-761, 'E', 763-841, 'M', 843, 'T', 845, 'N', 847-994 <CAM1>
A:Cross-references: EMBL:X70814; NID:g407778; PIDN:CAA50145.1; PID:g407779
A:Experimental source: non-proteolytic strain 2129B (Scott)
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, January 1993
A:Accession: S48104
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 634-843, 'T', 845, 'N', 847-994 <CAM2>
A:Cross-references: EMBL:X70819; NID:g407780; PIDN:CAA50150.1; PID:g407781
A:Experimental source: non-proteolytic strain Eklund 2B (Colworth 229)
C:Comment: Botulinum neurotoxin type B in these strains may possess a capable catalytic e
C:Genetics:
A:Gene: bont/b
C:Superfamily: tetanus toxin
C:Keywords: metalloprotein, neurotoxin, transmembrane protein, zinc
F:2-441/Product: botulinum neurotoxin type B light chain #status predicted <LIGHT>
F:442-1291/Product: botulinum neurotoxin type B heavy chain #status predicted <HVV>
F:230,234/Binding site: zinc (His) #status predicted

```

R;Schiavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B. Nature 359, 832-835, 1992
A:Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytically modifying synaptic vesicle proteins
A:Reference number: S27125; PMID:93063293; PMID:1331807
A:Contents: annotation
C:Comment: Botulinum neurotoxins inhibit neurotransmitter release from cholinergic synapses
C:Genetics:
A:Gene: bont/b
C:Function:
A:Description: catalyzes hydrolysis of a Gln-Phe peptide bond in synaptobrevin 2
C:Superfamily: tetanus toxin
C:Keywords: hydrolase; metalloproteinase; neurotoxin; transmembrane protein; zinc
P:2-441/Product: bontoxilysin B light chain #status experimental <LIGHT>
F:442-1291/Product: bontoxilysin B heavy chain #status experimental <HVY>
F:230,234/Binding site: zinc (His) #status predicted
F:231/Active site: Glu #status predicted

Query Match          23.0%; Score 63; DB 1; Length 1291;
Best Local Similarity 62.5%; Pred.No. 13;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy      15 SLFNFTVSVFLRVKPK 30
        |||:|||||:|||
Db       921 SVFLDSVSFWIRPK 936

RESULT 9
S46431
botulinum neurotoxin C1 - Clostridium botulinum phage 1C (strain C 468)
N:Alternate names: BoNT/C1 protein
C:Species: Clostridium botulinum phage 1C
A:Variety: strain C 468
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 16-Jul-1999
C:Accession: S46431; S49107
R:Hausser, D.; Eklund, M.W.; Boquet, P.; Popoff, M.R. Mol. Gen. Genet. 243, 631-640, 1994
A:Title: Organization of the botulinum neurotoxin C1 gene and its associated non-toxic A-subunit
A:Reference number: S46426; PMID:94301293; PMID:8028579
A:Accession: S46431
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1291 <HAU>
A:Cross-references: EMBL:X72793; NID:g516171; PIDN:CAA51313.1; PID:g516175
A:Experimental source: strain C 468
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, May 1993
C:Superfamily: tetanus toxin

Query Match          22.8%; Score 62.5; DB 2; Length 1291;
Best Local Similarity 25.4%; Pred.No. 15;
Matches 17; Conservative 13; Mismatches 12; Indels 25; Gaps 3;

Qy      5 YGLRPSSGP-----SLPNFTVSVFLRVKPVSAHLEGGPSL----- 41
        :   :   |||   :   :   :   :   :   :   :   :   :   :
Db       907 PDFKLGSSEGRGVIVTQNENIVNMYESFSISFWIRINK-WVSNLPGYTIIDSVKRN 965

Qy      42 -HWGYGL 47
        |||
Db       966 SGWSIGI 972

RESULT 10
A49777
botulinum neurotoxin type C1 precursor - Clostridium botulinum (type C, strain c-st)
C:Species: Clostridium botulinum
C:Date: 10-Mar-1994 #sequence_revision 07-Apr-1994 #text_change 17-Mar-2003
C:Accession: S11291; S45396; S22166; A49777
R:Hausser, D.; Eklund, M.W.; Kurazono, H.; Binz, T.; Niemann, H.; Gill, D.M.; Boquet, P. Nucleic Acids Res. 18, 4924, 1990
A:Title: Nucleotide sequence of Clostridium botulinum C1 neurotoxin.
A:Reference number: S11291; PMID:90370487; PMID:2204031
A:Accession: S11291
A>Status: preliminary
A:Molecule type: DNA

```

A;Residues: 1-84,'P',86-1291 <HAU>
 A;Cross-references: EMBL:X53751; NID:G14905; PIDN:CAA37780.1; PID:G14906
 R;Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Takeshi, K.
 Biochem. Biophys. Res. Commun. 171, 1304-1311, 1990
 A;Title: The complete nucleotide sequence of the gene coding for botulinum type C-1 toxin
 A;Reference number: A35396; MUID:91024998; PMID:2222445
 A;Accession: A35396
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: DNA
 A;Residues: 1-669,'R',671-1291 <TS1>
 R;Tsuzuki, K.; Kimura, K.; Fujii, N.; Yokosawa, N.; Oguma, K.
 submitted to the EMBL Data Library, December 1991
 A;Description: Nucleotide sequence of the gene for one of the components of hemagglutinin
 A;Reference number: S22163
 A;Accession: S22166
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-1291 <TS2>
 R;Kimura, K.; Fujii, N.; Tsuzuki, K.; Murakami, T.; Indoh, T.; Yokosawa, N.; Oguma, K.
 Appl. Environ. Microbiol. 57, 1168-1172, 1991
 A;Title: Cloning of the structural gene for Clostridium botulinum type C-1 toxin and who
 A;Reference number: A49777; MUID:91282468; PMID:2059039
 A;Accession: A49777
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-607 <TS3>
 A;Cross-references: GB:D90210
 C;Superfamily: tetanus toxin
 C;Keywords: neurotoxin

Query Match 22.8%; Score 62.5; DB 2; Length 1291;
 Best Local Similarity 25.4%; Pred. No. 15;
 Matches 17; Conservative 13; Mismatches 12; Indels 25; Gaps 3;
 QY 5 YGLRGSQSGP-----SLFNFTVSFWLRVFKVSAHLEGPSL----- 41
 DB 907 PDKLGSQSGEDRGKIVVQENIVNSVYFSFSFWLRINK-WVSNLPGLTIDSVKNN 965
 QY 42 -HWSYGL 47
 DB 966 SGWSIGI 972

RESULT 11
 I40645
 botulinum neurotoxin type A - Clostridium botulinum
 C;Species: Clostridium botulinum
 C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 16-Jul-1999
 C;Accession: I40645
 R;Willems, A.; East, A.K.; Lawson, P.A.; Collins, M.D.
 Res. Microbiol. 144, 547-556, 1993
 A;Title: Sequence of the gene coding for the neurotoxin of Clostridium botulinum type A
 A;Reference number: I40645; MUID:94143603; PMID:19310180
 A;Accession: I40645
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-1296 <RES>
 A;Cross-references: EMBL:X73423; NID:G507070; PIDN:CAA51824.1; PID:G507071
 C;Superfamily: tetanus toxin
 C;Keywords: neurotoxin

Query Match 22.6%; Score 62; DB 2; Length 1296;
 Best Local Similarity 50.0%; Pred. No. 18;
 Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 15 SLFNFTVSFWLRVFK 30
 DB 936 SMTENFSFWIKIPK 951

RESULT 12
 JC7393

medaka-type gonadotropin-releasing hormone precursor - Japanese medaka
 C;Species: Oryzias latipes (Japanese medaka)
 C;Date: 17-Nov-2000 #sequence_revision 17-Nov-2000 #text_change 20-Jan-2003
 C;Accession: JC7393
 R;Okubo, K.; Amano, M.; Yoshiura, Y.; Suetake, H.; Aida, K.
 Biochem. Biophys. Res. Commun. 276, 299-303, 2000
 A;Title: A novel form of gonadotropin-releasing hormone in the medaka, Oryzias latipes
 A;Reference number: JC7393
 A;Contents: Brain
 A;Accession: JC7393
 A;Molecule type: mRNA
 A;Residues: 1-91 <OKU>
 A;Cross-references: DDBJ:AB041333
 C;Comment: This protein plays the roles as a hypophysiotropic factor, and a physiologi
 C;Genetics:
 A;Gene: mdgnrh
 C;Superfamily: gonadoliberin
 C;Keywords: brain
 Query Match 22.4%; Score 61.5; DB 2; Length 91;
 Best Local Similarity 32.7%; Pred. No. 0.99;
 Matches 17; Conservative 7; Mismatches 23; Indels 5; Gaps 1;
 QY 2 HWSYGLRPGSSGPSLNNFTVSFWLRV-----PKVSASHLEGPSLHWSYGLR 48
 DB 23 HWSFGSLSPGKRELKFFNTLENQRLNLSNTPCSDLHLESLAKYIRIK 74
 RESULT 13
 RHRTG
 N;Alternase names: gonadoliberin-associated protein (GAP); gonadotropin releasing horm
 N;Contains: gonadoliberin; prolactin release-inhibiting factor
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999
 C;Accession: A40147; B26173; A48410
 R;Bond, C.T.; Hayflick, J.S.; Seeburg, P.H.; Adelman, J.P.
 Mol. Endocrinol. 3, 1257-1262, 1989
 A;Title: The rat gonadotropin-releasing hormone: SH locus: structure and hypothalamic
 A;Reference number: A40147; MUID:8938461; PMID:2476669
 A;Accession: A40147
 A;Molecule type: DNA
 A;Residues: 1-92 <BON>
 A;Cross-references: GB:M31670; NID:G204447; PIDN:AAA41264.1; PID:G204448
 R;Adelman, J.P.; Mason, A.J.; Hayflick, J.S.; Seeburg, P.H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 179-183, 1986
 A;Title: Isolation of the gene and hypothalamic cDNA for the common precursor of gonad
 A;Reference number: A94090; MUID:86094338; PMID:2867548
 A;Accession: B26173
 A;Molecule type: mRNA
 A;Residues: 1-92 <ADE>
 A;Cross-references: GB:M12579; NID:G204445; PIDN:AAA41263.1; PID:G204446
 R;Maier, C.C.; Marchetti, B.; LeBoeuf, R.D.; Blalock, J.E.
 Cell. Mol. Neurobiol. 12, 447-454, 1992
 A;Title: Thymocytes express a mRNA that is identical to hypothalamic luteinizing hormo
 A;Reference number: A48410; MUID:93105480; PMID:1468115
 A;Accession: A48410
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-92 <MAI>
 A;Cross-references: GB:S50870; NID:G262059; PIDN:AA824572.1; PID:G262060
 A;Experimental source: thymus
 A;Note: sequence extracted from NCBI backbone (NCBIN:121082, NCBI:P:121083)
 C;Genetics:
 A;Introns: 47/3; 79/3
 C;Function:
 A;Description: stimulates pituitary secretion of lutropin and follitropin
 A;Note: gonadoliberin-associated protein may have prolactin release inhibiting activity
 C;Superfamily: gonadoliberin
 C;Keywords: amidated carboxyl end; hormone; hypothalamus; placenta; pyroglutamic acid;
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;24-92/Product: progadoliberin #status predicted <PGN>
 F;24-93/Product: gonadoliberin #status predicted <GLN>

Job time : 16.623 secs

F;37-92/Product: prolactin release-inhibiting factor #status predicted <PIP>
F;24/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted
F;33/Modified site: amidated carboxyl end (Gly) (amide in mature form from following gly

Query Match 22.4%; Score 61.5; DB 1; Length 92;
Best Local Similarity 51.7%; Pred. No. 1;
Matches 15; Conservative 3; Mismatches 4; Indels 7; Gaps 2;

QY 28 VPKVSAS-----HLEG-PSLHWSYGLRP 49
: : : : :
Db 4 IPKMAAVLLTVCLGCSQHSYGLRP 32

RESULT 14

S48110
neurotoxin type F - Clostridium botulinum (fragment)
C/Species: Clostridium botulinum
C/Date: 14-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C/Accession: S48110
R/Campbell, K.D.; Collins, M.D.; East, A.K.
J. Clin. Microbiol. 31, 2255-2262, 1993
A/Title: Gene probes for identification of the botulinum neurotoxin gene and specific id
A/Reference number: S48103; MUID:94013372; PMID:8408542
A/Accession: S48110
A/Status: preliminary; translation not shown
A/Molecule type: DNA
A/Residues: 1-366 <CAM>
A/Cross-references: EMBL:X70821; NID:g407792; PIDN:CAA50152.1; PID:g407793
C/Superfamily: tetanus toxin
C/Keywords: neurotoxin

Query Match 22.3%; Score 61; DB 2; Length 366;
Best Local Similarity 57.1%; Pred. No. 5.6;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 17 FNNFTVSFWLRVPK 30
: : : : :
Db 297 YQNFISFWVRPK 310

RESULT 15

T36589
probable transmembrane protein - Streptomyces coelicolor
C/Species: Streptomyces coelicolor
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Aug-2000
C/Accession: T36589
R/Oliver, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, May 1999
A/Reference number: Z21575
A/Accession: T36589
A/Status: preliminary; translated from GB/EMBL/DDBJ
A/Molecule type: DNA
A/Residues: 1-502 <OLI>
A/Cross-references: EMBL:AL049826; PIDN:CAB42730.1; GSPDB:GNO0070; SCOEDB:SCH24.24
A/Experimental source: strain A3(2)
C/Genetics:
A/Gene: SCOEDB:SCH24.24
C/Superfamily: Mycobacterium tuberculosis probable membrane protein Rv0051

Query Match 22.3%; Score 61; DB 2; Length 502;
Best Local Similarity 24.1%; Pred. No. 8;
Matches 19; Conservative 7; Mismatches 21; Indels 32; Gaps 3;

QY 2 HWSYGL-----RPGSSGPS-----LFNNFTVSFWLRVPK 30
: : : : :
Db 421 HWAIGLHLGLTFLCAMVVRDILMPDRDPVRRRTGDDDDPSGGVLDGAEDVFLGPAARTER 480

QY 31 VSASHLEGPSLHWSYGLRP 49
: : : : :
Db 481 PTA-HFEGPQVHWGKGRQP 498

Search completed: March 10, 2004, 09:16:52

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:53 ; Search time 9.14397 Seconds
(without alignments)
284.724 Million cell updates/sec

Title: US-09-848-834A-18

Perfect score: 274

Sequence: 1 XHWSYGLRPGSGPSLFNFF.....VSASHLEGPSTLWSYGLRXP 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 segs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	41.6	1314	1	TETX_CLOTE
2	67	24.5	1296	1	BXG_CLOBO
3	65	23.7	1295	1	BXA1_CLOBO
4	63	23.0	431	1	PURA_LEGPN
5	63	23.0	1274	1	EXF_CLOBO
6	63	23.0	1290	1	EXB_CLOBO
7	62.5	22.8	1290	1	EXC1_CLOBO
8	62	22.6	1051	1	VP2_AHSV6
9	62	22.6	1295	1	BXA2_CLOBO
10	61.5	22.4	91	1	GON1_ORVLA
11	61.5	22.4	92	1	GON1_RAT
12	60	21.9	92	1	GON1_TUPGB
13	59	21.5	67	1	GON1_MACNU
14	59	21.5	92	1	GON1_HUMAN
15	58.5	21.4	1250	1	EXE_CLOBO
16	58	21.2	61	1	GON1_SHREP
17	58	21.2	63	1	GON1_MESAU
18	58	21.2	89	1	GON1_XENLA
19	58	21.2	90	1	GON1_MOUSE
20	58	21.2	90	1	GON1_RANCA
21	58	21.2	91	1	GON1_PIG
22	57.5	21.0	352	1	COA2_SV40
23	57.5	21.0	842	1	ASBC_HUMAN
24	56.5	20.6	94	1	GON1_HAPBU
25	56.5	20.6	551	1	SVK_BRUME
26	56.5	20.6	551	1	SVK_BRUSU
27	56.5	20.6	658	1	STC1_STAAU
28	56.5	20.6	1250	1	EXE_CLOBO
29	56	20.4	92	1	GON1_CHICK
30	56	20.4	141	1	AMPM_MYCCA
31	56	20.4	469	1	CG51_HUMAN
32	55.5	20.3	549	1	FIXN_BRAJA
33	55.5	20.3	715	1	STC2_STAAU

34 54.5 19.9 464 1 VNSS_TSWV1
35 54.5 19.9 3122 1 DPOZ_MOUSE
36 54.5 19.9 5217 1 HTS1_COCCA
37 54 19.7 10 1 GON1_ALIMI
38 54 19.7 585 1 YH70_SYNY3
39 53.5 19.5 536 1 OPGD_XYLFY
40 53.5 19.5 654 1 PSTA_MYCGB
41 53.5 19.5 760 1 AMY_GLOAB
42 53 19.3 99 1 GON1_DICUA
43 53 19.3 449 1 VNSS_INSVN
44 53 19.3 746 1 PFEA_PSEAB
45 53 19.3 1196 1 BXCN_CLOBO

ALIGNMENTS

RESULT 1
TETX_CLOTE
ID TETX_CLOTE STANDARD; PRT; 1314 AA.
AC P04958;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tetanus toxin precursor (EC 3.4.24.68) (Tentoxylisin) [Contains:
DE Tetanus toxin light chain (Tetanus toxin chain L); Tetanus toxin heavy
DE chain (Tetanus toxin chain H)].
GN TETX OR CTP60.
OS Clostridium tetani.
OG Plasmid pE88, and Plasmid 75 Kbp.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
NCBI_TaxID=1513;
RX [1]
RP SEQUENCE FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=87053814; PubMed=336478;
RA Eisel U., Jarausch W., Goretzki K., Henschen A., Engels J.,
RA Weller U., Hudel M., Habermann E., Niemann H.;
RT "Tetanus toxin: primary structure, expression in E. coli, and
RT homology with botulinum toxins.";
EMBO J. 5:2495-2502(1986).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CN3911; PLASMID=75 Kbp;
RX MEDLINE=87040747; PubMed=3774547;
RA Fairweather N.F., Lyness V.A.;
RT "The complete nucleotide sequence of tetanus toxin.";
RN Nucleic Acids Res. 14:7809-7812(1986).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Massachusetts / E88; PLASMID=pE88;
RX MEDLINE=22457253; PubMed=12552129;
RA Brueggemann H., Baeumer S., Fricke W.F., Wiezer A., Liesegang H.,
RA Decker I., Hezberg C., Martinez-Arias R., Merkl R., Henne A.,
RA Gottschalk G.;
RT "The genome sequence of Clostridium tetani, the causative agent of
RT tetanus disease.";
Proc. Natl. Acad. Sci. U.S.A. 100:1316-1321(2003).
RN [4]
RP SEQUENCE OF 742-1314 FROM N.A.
RC PLASMID=75 Kbp;
RX MEDLINE=86085572; PubMed=3510167;
RA Fairweather N.F., Lyness V.A., Pickard D.J., Allen G., Thomson R.O.;
RT "Cloning, nucleotide sequencing, and expression of tetanus toxin
RT fragment C in Escherichia coli.";
J. Bacteriol. 165:21-27(1986).
RN [5]
RP PARTIAL SEQUENCE, AND DISULFIDE BONDS.
RX MEDLINE=90201034; PubMed=2108021;
RA Krieglstein K., Henschen A., Weller U., Habermann E.;
RT "Arrangement of disulfide bridges and positions of sulfhydryl groups
RT in tetanus toxin.";

P26002 tomato spot
Q61493 mus musculu
Q01886 cochliobolu
P37041 alligator m
P73627 synechocyst
Q87927 xylella fas
P47651 mycoplasma
P23671 clostridium
Q91a10 dicentrarch
Q01811 impatiens n
Q05098 pseudomonas
P46081 clostridium

RL Eur. J. Biochem. 188:39-45(1990).
 RN [6]
 RP PARTIAL SEQUENCE.
 RX MEDLINE=92037649; PubMed=1935979;
 RA Krieglstein K.G., Henchen A.H., Weller U., Habermann E.;
 RT "limited proteolysis of tetanus toxin. Relation to activity and
 FT identification of cleavage sites.";
 RN Eur. J. Biochem. 202:41-51(1991).
 RP [7]
 RX IDENTIFICATION AS ZINC-PROTEASE.
 RA Schiavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
 RA Montecucco C.;
 RT "tetanus toxin is a zinc protein and its inhibition of
 RT neurotransmitter release and protease activity depend on zinc.";
 RN EMBO J. 11:3577-3583(1992).
 RP [8]
 RX IDENTIFICATION OF SUBSTRATE.
 RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
 RA Daugupta B.R., Montecucco C.;
 RT "tetanus and botulinum-B neurotoxins block neurotransmitter release
 RT by proteolytic cleavage of synaptobrevin.";
 RN Nature 359:832-835(1992).
 RP [9]
 RX X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
 RA MEDLINE=97475247; PubMed=9334741;
 RA Unland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
 RA Sax M.;
 RT "Structure of the receptor binding fragment HC of tetanus
 RT neurotoxin.";
 RN Nat. Struct. Biol. 4:788-792(1997).
 RP CC -|- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
 CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
 CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
 CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
 CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
 CC ENDOPEPTIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-77
 CC BOND OF SYNAPTOSOMAL-2.
 CC -|- CATALYTIC ACTIVITY: Hydrolysis of 76-Gln-|-Phe-77 bond in
 CC synaptobrevin 2.
 CC -|- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -|- SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO
 CC YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE
 CC AND ARE NON-TOXIC AFTER SEPARATION.
 CC -|- MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
 CC GANGLIOSIDE RECEPTORS.
 CC -|- SIMILARITY: Belongs to peptidase family M27.
 CC -----
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 CC -----
 CC EMBL; X04436; CAA28033.1; -;
 CC EMBL; X06214; CAA29564.1; -;
 CC EMBL; AF528097; AAC37454.1; -;
 CC EMBL; M12739; AAA23282.1; -;
 CC PIR; A25689; BTCLTN.
 CC PDB; 1AF9; 29-APR-98.
 CC PDB; 1A8D; 14-OCT-98.
 CC PDB; 1DOH; 27-MAR-00.
 CC PDB; 1DFQ; 24-MAR-00.
 CC PDB; 1DIW; 24-MAR-00.
 CC PDB; 1DLL; 24-MAR-00.
 CC PDB; 1FV3; 05-SEP-01.
 CC MEROPS; M27.001; -;
 CC InterPro; IPR008985; ConA like lec.gl.
 CC InterPro; IPR002160; Kunitz legume.
 CC InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR000395; Peptidase M27.
 DR Pfam; PF01742; Peptidase M27; 1.
 DR PRINTS; PR00760; BONTOKILYSIN.
 DR ProDom; PD001963; Bontoxilysin; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE_1.
 DR Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc; Plasmid;
 KW 3D-structure; Complete proteome.
 FT INIT MET 0
 FT CHAIN 1 456
 FT METAL 457 1314
 FT ACT SITE 232 233
 FT METAL 236 236
 FT TRANSMEM 226 246
 FT DISULFID 438 466
 FT DISULFID 1076 1092
 FT HELIX 876 882
 FT TURN 883 883
 FT STRAND 884 891
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 FT STRAND 909 910
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 FT STRAND 920 925
 FT TURN 928 929
 FT STRAND 932 935
 FT HELIX 938 940
 FT TURN 941 946
 FT STRAND 949 956
 FT HELIX 962 968
 FT TURN 969 970
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 FT STRAND 980 981
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 FT TURN 1116 1117
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 FT TURN 1122 1122
 FT STRAND 1124 1124
 FT TURN 1127 1131
 FT STRAND 1132 1134
 FT TURN 1135 1136
 FT STRAND 1137 1141
 FT TURN 1144 1145
 FT STRAND 1148 1152
 FT TURN 1155 1158
 FT STRAND 1159 1162
 FT TURN 1163 1166
 FT STRAND 1173 1178
 FT TURN 1184 1185
 FT STRAND 1188 1188
 FT STRAND 1190 1190
 FT TETANUS TOXIN LIGHT CHAIN.
 FT TETANUS TOXIN HEAVY CHAIN.
 FT ZINC (CATALYTIC) (BY SIMILARITY).
 FT BY SIMILARITY.
 FT ZINC (CATALYTIC) (BY SIMILARITY).
 FT POTENTIAL.
 FT INTERCHAIN.

RA FUJILC

FT
INT

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neurocokin; hydrolase; metalloprotease; zinc.
INIT_MET      0      0
BY SIMILARITY.
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"Molecular characterization of two forms of nontoxic-nonhemagglutinin components of Clostridium botulinum type A progenitor toxins.";
RT FBES Lett. 376:41-44(1995).
RN [6]
RP SEQUENCE OF 1-16.
RX MEDLINE=94178501; PubMed=6370252;
RA Schmidt J.J., Sartymoorthy V., Dasgupta B.R.;
RT "Partial amino acid sequence of the heavy and light chains of
RT botulinum neurotoxin type A.";
RL Biochem. Biophys. Res. Commun. 119:900-904(1984).
RN [7]
RP SEQUENCE OF 1-46.
RX Dasgupta B.R., Foley J., Niece R.;
RA "Partial sequence of the light chain of botulinum neurotoxin type A.";
RL Biochemistry 26:4162-4162(1987).
RN [8]
RP SEQUENCE OF 1-5 AND 444-456.
RX MEDLINE=91120847; PubMed=2126206;
RA Dasgupta B.R., Dekleva M.L.;
RT "Botulinum neurotoxin type A: sequence of amino acids at the
RT N-terminus and around the nicking site.";
RL Biochimie 72:661-664(1990).
RN [9]
RP SEQUENCE OF 448-464 AND 872-895.
RX MEDLINE=89024662; PubMed=3178218;
RA Sathymoorthy V., Dasgupta B.R., Foley J., Niece R.L.;
RT "Botulinum neurotoxin type A: cleavage of the heavy chain into two
RT halves and their partial sequences.";
RL Arch. Biochem. Biophys. 266:142-151(1988).
RN [10]
RP SEQUENCE OF 448-482.
RX MEDLINE=85285016; PubMed=3896784;
RA Shone C.C., Hambleton P., Melling J.;
RT "Inactivation of Clostridium botulinum type A neurotoxin by trypsin
RT and purification of two tryptic fragments. Proteolytic action near
RT the COOH-terminus of the heavy subunit destroys toxin-binding
RT activity.";
RL Eur. J. Biochem. 151:75-82(1985).
RN [11]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94063091; PubMed=8243676;
RA Benfenati G., Santucci A., Dasgupta B.R., Mehta P.P., Jontes J.,
RT "Botulinum neurotoxins serotypes A and E cleave SNAP-25 at distinct
RT COOH-terminal peptide bonds.";
RL FBES Lett. 335:99-103(1993).
RN [12]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94124495; PubMed=8294407;
RA Binz T., Blasi J., Yamasaki S., Baumeister A., Link E., Suedhof T.C.,
RT "Proteolysis of SNAP-25 by types E and A botulinum neurotoxins.";
RL J. Biol. Chem. 269:1617-1620(1994).
RN [13]
RP MUTAGENESIS OF GLU-261; PHE-265 AND TYR-365.
RX MEDLINE=21556941; PubMed=11700044;
RA Rigoni M., Caccini P., Johnson E.A., Montecucco C., Rossetto O.;
RT "Site-directed mutagenesis identifies active-site residues of the
RT light chain of botulinum neurotoxin type A.";
RL Biochem. Biophys. Res. Commun. 288:1231-1237(2001).
RN [14]
RP X-RAY CRYSTALLOGRAPHY (3.3 ANGSTROMS).
RX MEDLINE=98455071; PubMed=9783750;
RA Lacy D.B., Tepp W., Cohen A.C., Dasgupta B.R., Stevens R.C.;
RT "Crystal structure of botulinum neurotoxin type A and implications
RT for toxicity.";
RL Nat. Struct. Biol. 5:898-902(1998).
CC -1- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
CC binds with high affinity to peripheral neuronal presynaptic
CC membrane, is then internalized by receptor-mediated endocytosis.
CC The C-terminus of the heavy chain (H) is responsible for the
CC adherence of the toxin to the cell surface while the N-terminus
CC mediates transport of the light chain from the endocytic vesicle

to the cytosol. After translocation, the light chain (L)
hydrolyzes the 197-Gln-Arg-198 bond in SNAP-25, thereby blocking
neurotransmitter release. Inhibition of acetylcholine release
results in flaccid paralysis, with frequent heart or respiratory
failure.
-1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
neurexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
detected action on small molecule substrates.
-1- COFACTOR: Binds 1 zinc ion per subunit.
-1- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
heavy chain (H).
-1- SUBCELLULAR LOCATION: Secreted.
-1- PHARMACEUTICAL: Available under the name BOTOX (Allergan) for
the treatment of strabismus and blepharospasm associated with
dystonia and cervical dystonia. Also used for the treatment of
hemifacial spasm and a number of other neurological disorders
characterized by abnormal muscle contraction.
-1- MISCELLANEOUS: There are seven antigenically distinct forms of
botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
-1- SIMILARITY: Belongs to peptidase family M27.
-1- DATABASE: NAME=BOTOX product information Web site;
WWW=http://www.botox.com/index.jsp?hp&productinfo".
-1- DATABASE: NAME=protein Spotlight;
NOTE=Issue 19 of February 2002;
WWW=http://www.expasy.org/spotlight/articles/sptlt019.html".

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EMBL; X52066; CAA36289.1; -
EMBL; M30196; AAA23262.1; -
EMBL; X92973; CAA63551.1; -
EMBL; D67030; BAA11051.1; -
EMBL; M27892; AAA23269.1; -
PIR; A35294; BTCLAB.
PDB; 3BTA; 01-OCT-99.
MEROPS; M27.002; -
InterPro; IPR008985; ConA like lec_gl.
InterPro; IPR002160; Kunitz legume.
InterPro; IPR006025; Pept_M_zn_BS.
InterPro; IPR000395; Peptidase M27.
Pfam; PF01742; Peptidase M27; 1.
PRINTS; PR00760; BONTOKILYSIN.
ProDom; PD001963; Bontoxilysin; 1.
PROSITE; PS00142; ZINC_PROTEASE; 1.
Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc;
Pharmaceutical; 3D-structure.
INIT MET 0 0
FT CHAIN 1 447 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
FT CHAIN 448 1295 BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
FT METAL 222 222 ZINC (CATALYTIC).
FT ACT SITE 223 223 ZINC (CATALYTIC).
FT METAL 226 226 ZINC (CATALYTIC).
FT METAL 261 261 ZINC (CATALYTIC).
FT DISULFID 429 453 INTERCHAIN.
FT DISULFID 1234 1279
FT TRANSMEM 626 646
FT TRANSMEM 655 675
FT VARIANT 26 26
FT MUTAGEN 261 261
FT MUTAGEN 265 265
FT MUTAGEN 365 365
FT CONFLICT 1 1
FT CONFLICT 479 479
FT CONFLICT 875 875
FT CONFLICT 891 891
FT SEQUENCE 1295 AA; 149322 MW; 858342F754862579 CRC64;

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CC ENBL; M92906; AAA23263.1; -
CC ENBL; S73676; AAC60475.1; -
CC ENBL; X70820; CAA50151.1; -
CC ENBL; X70816; CAA50147.1; -
CC PIR; I40813; I40813.
CC PIR; S48109; S48109.
CC HSP; P10845; 3BTA.
CC MEROPS; M27.002; -.
CC InterPro; IPR008985; ConA like lec.gl.
CC InterPro; IPR002180; Kunitz legume.
CC InterPro; IPR006025; Pept_M_Zn_BS.
CC InterPro; IPR000395; Peptidase M27.
CC Pfam; PF01742; Peptidase M27; 1.
CC PRINTS; PR00760; BONTOKILYSIN.
CC PRODOM; PD001963; Bontoxilysin; 1.
CC Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
CC CHAIN 1 435 BOTULINUM NEUROTOXIN F, LIGHT-CHAIN.
CC CHAIN 437 1274 BOTULINUM NEUROTOXIN F, HEAVY-CHAIN.
CC METAL 227 227 ZINC (CATALYTIC) (BY SIMILARITY).
CC ACT_SITE 228 228 BY SIMILARITY.
CC METAL 231 231 ZINC (CATALYTIC) (BY SIMILARITY).
CC FT D-SULFID 429 445 INTERCHAIN (PROBABLE).
CC SEQUENCE 1274 AA; 146709 MW; 5B99756A7438B921 CRC64;

Query Match 23.0%; Score 63; DB 1; Length 1274;
Best Local Similarity 56.2%; Pred. No. 7.7;
Matches 9; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 15 SLFNNFTVSFWLRVPK 30
Db 928 SRVGNFSISFWLRPK 943

RESULT 6
BXE_CLOBO STANDARD; PRT; 1290 AA.
AC P10844; P10843;
DT 01-JUL-1989 (Rel. 11, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Botulinum neurotoxin type B precursor (EC 3.4.24.69) (BoNT/B)
DE (Bontoxilysin B).
GN BOTB.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium
OC NCBI_TaxID=1491;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92384550; PubMed=1514783;
RA Whelan S.M., Elmore M.J., Bodsworth N.J., Brehm J.K., Atkinson T.,
RA Minton N.P.;
RT "Molecular cloning of the Clostridium botulinum structural gene
RT encoding the type B neurotoxin and determination of its entire
RT nucleotide sequence."
RL Appl. Environ. Microbiol. 58:2345-2354 (1992).
RN [2]
RP SEQUENCE OF 35-245 FROM N.A.
RC STRAIN=NCTC 7273;
RA Szabo E.A., Pemberton J.M., Desmarchelier P.M.;
RA Submitted (APR-1992) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 633-993 FROM N.A.
RC STRAIN=NCTC 7273;
RX MEDLINE=94013372; PubMed=8408542;
RA Campbell K., East A.K., Collins M.D.;
RT "Gene probes for identification of the botulinum neurotoxin gene and
RT specific identification of neurotoxin types B, E, and F."

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RL J. Clin. Microbiol. 31:2255-2262 (1993).
RN [4]
RP SEQUENCE OF 1-44 AND 441-466.
RC STRAIN=657;
RX MEDLINE=89000987; PubMed=3139097;
RA Dasgupta B.R., Datta A.;
RT "Botulinum neurotoxin type B (strain 657): partial sequence and
RT similarity with tetanus toxin."
RL Biochimie 70:811-817 (1988).
RN [5]
RP SEQUENCE OF 1-16 AND 441-458.
RC STRAIN=OKRA;
RX MEDLINE=85197963; PubMed=3888113;
RA Schmidt J.J., Sathiyamoorthy V., Dasgupta B.R.;
RT "Partial amino acid sequences of botulinum neurotoxins types B and
RT E."
RL Arch. Biochem. Biophys. 238:544-548 (1985).
RN [6]
RP IDENTIFICATION AS ZINC-PROTEASE.
RX MEDLINE=93054694; PubMed=1429690;
RA Schiavo G., Rossetto O., Santucci A., Dasgupta B.R., Montecucco C.;
RL J. Biol. Chem. 267:23479-23483 (1992).
RN [7]
RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=93063293; PubMed=1331807;
RA Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P.,
RL "Tetanus and botulinum-B neurotoxins block neurotransmitter release
RT by proteolytic cleavage of synaptobrevin."
CC Nature 359:832-835 (1992).
CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CLEAVES THE 76-GLN-|-PHE-77 BOND OF
CC SYNAPTOSOMAL-2.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
CC -!- SIMILARITY: Belongs to peptidase family M27.
CC -----
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CC EMBL; M81186; AAA23211.1; -
CC EMBL; Z11934; CAA77991.1; -
CC EMBL; X70817; CAA50148.1; -
CC PIR; A48940; A48940.
CC PDB; IEPW; 01-NOV-00.
CC PDB; IF31; 01-NOV-00.
CC PDB; IF82; 16-AUG-00.
CC PDB; IF83; 16-AUG-00.
CC PDB; IFQ8; 08-DEC-00.
CC PDB; IG9A; 13-NOV-00.
CC PDB; IG9B; 13-NOV-02.
CC PDB; IG9D; 13-NOV-02.
CC PDB; I11E; 21-NOV-01.

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DR MEOPS; M27.002; -.
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOKILYSIN.
DR ProDom; PD001963; Bontokilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; transmembrane; Hydrolase; Metalloprotease; Zinc;
KW 3D-structure.
FT INIT_MET 0
FT CHAIN 1 440
FT CHAIN 441 1290
FT METAL 229
FT ACT_SITE 230
FT METAL 233
FT DISULFID 436
FT CONFLICT 29
FT CONFLICT 217
FT CONFLICT 224
FT CONFLICT 463
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Query Match 23.0%; Score 63; DB 1; Length 1290;
Best Local Similarity 62.5%; Pred. No. 7.8;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 15 SLFNNFTSVFLRVK 30
DB 920 SVFLDFSVFWIRPK 935
RESULT 7
EX1_CLOBO STANDARD; PRT; 1290 AA.
AC P18640;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type C1 precursor (EC 3.4.24.69) (BoNT/C1)
DE (Bontokilysin C1).
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90370487; PubMed=2204031;
RA Hauser D., Eklund M.W., Kurazona H., Binz T., Niemann H., Gill D.M.,
RA Boruet P., Popoff M.R.;
PT "Nucleotide sequence of Clostridium botulinum C1 neurotoxin.";
RL Nucleic Acids Res. 18:4924-4924(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Type C Stockholm / C-ST;
RX MEDLINE=91024998; PubMed=222445;
RA Kimura K., Fujii N., Tsuzuki K., Murakami T., Indoh T.,
RA Yokosawa N., Takeshi K., Syuto B., Oguma K.;
RT "The complete nucleotide sequence of the gene coding for botulinum
RT type C1 toxin in the C-ST phage genome.";
RL Biochem. Biophys. Res. Commun. 171:1304-1311(1990).
RN [3]
RP SEQUENCE OF 2-25.
RX STRAIN=Type C Stockholm / C-ST;
RX MEDLINE=88153072; PubMed=2450068;
RA Tsuzuki K., Yokosawa N., Syuto B., Ohishi I., Fujii N., Kimura K.,
RA Oguma K.;
RT "Establishment of a monoclonal antibody recognizing an antigenic site
RT common to Clostridium botulinum type B, C1, D, and E toxins and
RL tetanus toxin.";
RL Infect. Immun. 56:898-902(1988).
RN [4]

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RP IDENTIFICATION OF SUBSTRATE.
RX MEDLINE=94038966; PubMed=7901002;
RT Blasi J., Chapman E.R., Yamasaki S., Binz T., Niemann H., Jahn R.;
RT "Botulinum neurotoxin C1 blocks neurotransmitter release by means of
RT cleaving HPC-1/syntaxin.";
RL EMBO J. 12:4821-4828(1993).
CC -!- FUNCTION: BOTULINUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
CC RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
CC AND MOVES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
CC WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
CC INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
CC ENDOPEPTIDASE THAT CLEAVES SYNTAXIN.
CC -!- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H). The light chain has the pharmacological activity,
CC while the N- and C-terminal of the heavy chain mediate channel
CC formation and toxin binding, respectively.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F and G.
CC -!- MISCELLANEOUS: BOTULINUM TYPE C1 NEUROTOXIN IS SYNTHESIZED BY C
CC STRAIN OF CLOSTRIDIUM BOTULINUM WHICH CARRY THE APPROPRIATE
CC BACTERIOPHAGE.
CC -!- SIMILARITY: Belongs to peptidase family M27.
CC
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CC
CC EMBL; X66433; CAA47060.1; -
CC EMBL; X72933; CAA51313.1; -
CC EMBL; X53751; CAA37780.1; -
CC EMBL; D90210; BAA14235.1; -
CC EMBL; X62389; CAA44263.1; -
CC HSP; P10845; 3BTA.
CC MEROPS; M27.002; -.
DR InterPro; IPR008985; ConA_like lec_gl.
DR InterPro; IPR002160; Kunitz_legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR InterPro; IPR000395; Peptidase_M27.
DR Pfam; PF01742; Peptidase_M27; 1.
DR PRINTS; PR00760; BONTOKILYSIN.
DR ProDom; PD001963; Bontokilysin; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; 1.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT_MET 0
FT CHAIN 1 448
FT CHAIN 449 1290
FT METAL 228
FT ACT_SITE 229
FT METAL 232
FT DISULFID 436
FT CONFLICT 84
FT SEQUENCE 1290 AA; 148734 MW; 71FBE379F97129E8 CRC64;
Query Match 22.8%; Score 62.5; DB 1; Length 1290;
Best Local Similarity 25.4%; Pred. No. 9;
Matches 17; Conservative 13; Mismatches 12; Indels 25; Gaps 3;
QY 5 VGLRGSSGP-----SLFNNFTSVFLRVKVSASHLEGPSL-----41
DB 906 FDFKLGGSGEDRGKVIYTONENIVNMYESFSISFWIRNK-WVSNLPGYTIIDSVKN 964
QY 42 -HWSYGL 47
DB 965 SCWSIGI 971

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RESULT 8
ID VP2_AHSV6 STANDARD; PRT; 1051 AA.
AC OVI024;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Outer capsid protein VP2.
GN S2 OR L2.
OS African horse sickness virus 6 (AHSV-6) (African horse sickness virus
OS (serotype 6)).
OC Viruses; dsRNA viruses; Reoviridae; Orbivirus.
OX NCBI_TaxID=86060;
RN [1]
RP MEDLINE=98278311; PubMed=9617769;
RX Williams C.F., Inoue T., Lucas A.-M., Zanotto P., Roy P.;
RA "The complete sequence of four major structural proteins of African
RT horse sickness virus serotype 6: evolutionary relationships within
RT and between the orbiviruses."
RL Virus Res. 53:53-73(1998).
CC -1- FUNCTION: THE VP2 PROTEIN IS ONE OF THE TWO PROTEINS (WITH VP5)
CC WHICH CONSTITUTE THE VIRUS PARTICLE OUTER CAPSID. IT IS THE
CC MAJOR TARGET OF THE HOST IMMUNOGENIC RESPONSE.
CC -1- SIMILARITY: Belongs to the reoviruses VP2 protein family.
CC -----
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CC -----
EMBL; AF021235; AAC40994.1; -.
DR InterPro; IPR001742; Orbi_VP2.
DR Pfam; PF00898; Orbi_VP2; 1.
DR KW Coat protein.
SQ SEQUENCE 1051 AA; 122326 MW; 2B04DB9B389F4B5F CRC64;

Query Match 22.6%; Score 62; DB 1; Length 1051;
Best Local Similarity 40.7%; Pred. No. 8.2;
Matches 11; Conservative 6; Mismatches 10; Indels 0; Gaps 0;

QY 11 SSGPSLFNNFTVGFWRVVKVASHLE 37
Db 630 TEGVTYFSKRFVSYWRVEKITTKHLE 656

RESULT 9
ID BXA2_CLOBO STANDARD; PRT; 1295 AA.
AC Q45894; P77780;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Botulinum neurotoxin type A precursor (EC 3.4.24.69) (BoNT/A)
DE (Bontoxilysin A) (BOROX) [Contains: Botulinum neurotoxin A, light-
DE chain; Botulinum neurotoxin A, heavy-chain].
GN BOTA OR BNA OR ATX.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Kyoto-F;
RX MEDLINE=94143603; PubMed=8310180;
RA Williams A., East A.K., Lawson P.A., Collins M.D.;
RT "Sequence of the gene coding for the neurotoxin of Clostridium
RT botulinum type A associated with infant botulism: comparison with

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other clostridial neurotoxins.";
Res. Microbiol. 144:547-556(1993).
[2]
RP SEQUENCE OF 1-65 FROM N.A.
RC STRAIN=Kyoto-F;
RX MEDLINE=97016817; PubMed=8863443;
RA East A.K., Bhandari M., Stacey J.M., Campbell K.D., Collins M.D.;
RT "Organization and phylogenetic interrelationships of genes encoding
RT components of the botulinum toxin complex in proteolytic Clostridium
RT botulinum types A, B, and F: evidence of chimeric sequences in the
RT gene encoding the nontoxic nonhemagglutinin component.";
Int. J. Syst. Bacteriol. 46:1105-1112(1996).
CC -1- FUNCTION: Inhibits acetylcholine release. The botulinum toxin
CC binds with high affinity to peripheral neuronal presynaptic
CC membrane, is then internalized by receptor-mediated endocytosis.
CC the C-terminus of the heavy chain (H) is responsible for the
CC adherence of the toxin to the cell surface while the N-terminus
CC mediates transport of the toxin to the light chain from the endocytic vesicle
CC to the cytosol. After translocation, the light chain (L)
CC hydrolyzes the 197-Gln-|-Arg-198 bond in SNAP-25, thereby blocking
CC neurotransmitter release. Inhibition of acetylcholine release
CC results in flaccid paralysis, with frequent heart or respiratory
CC failure (By similarity).
CC -1- CATALYTIC ACTIVITY: Limited hydrolysis of proteins of the
CC neuroexocytosis apparatus, synaptobrevins, SNAP25 or syntaxin. No
CC detected action on small molecule substrates.
CC -1- SUBUNIT: Disulfide-linked heterodimer of a light chain (L) and a
CC heavy chain (H) (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: There are seven antigenically distinct forms of
CC botulinum neurotoxin: Types A, B, C1, D, E, F, and G.
CC -1- SIMILARITY: Belongs to peptidase family M27.
CC -----
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CC -----
EMBL; X73423; CAA51824.1; -.
DR EMBL; X87974; CAA61234.1; -.
DR PIR; I40645; I40645.
DR HSSP; P10845; 3BTA.
DR MEROPS; M27.002; -.
DR InterPro; IPR008985; ConA like lec.gl.
DR InterPro; IPR002160; Kunitz legume.
DR InterPro; IPR006025; Pept_M_Zn_BS.
DR Pfam; PF01742; Peptidase_M27.
DR PRINTS; PR00760; BONTXILYSIN.
DR ProDom; PD001963; Bontoxilysin; 1.
DR PROSITE; PS00142; ZINC PROTEASE; FALSE NEG.
KW Neurotoxin; Transmembrane; Hydrolase; Metalloprotease; Zinc.
FT INIT MET 0 0 BY SIMILARITY.
FT CHAIN 1 447 BOTULINUM NEUROTOXIN A, LIGHT-CHAIN.
FT METAL 448 1295 BOTULINUM NEUROTOXIN A, HEAVY-CHAIN.
FT ACT SITE 222 222 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT SITE 223 223 BY SIMILARITY.
FT METAL 226 226 ZINC (CATALYTIC) (BY SIMILARITY).
FT DISULFID 429 453 INTERCHAIN (BY SIMILARITY).
FT DISULFID 1234 1279 BY SIMILARITY.
FT TRANSMEM 626 646 POTENTIAL.
FT TRANSMEM 655 675 POTENTIAL.
SQ SEQUENCE 1295 AA; 149279 MW; 5DA04A19D98D6372 CRC64;

Query Match 22.6%; Score 62; DB 1; Length 1295;
Best Local Similarity 50.0%; Pred. No. 10;
Matches 8; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 15 SLFNNFTVGFWRVVKV 30
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CC
 CC EMBL; S50870; AAB24572.1; -;
 CC EMBL; M12579; AAA41263.1; -;
 CC EMBL; M31670; AAA41264.1; -;
 CC EMBL; M15527; AAA42141.1; ALT_SEQ.
 CC EMBL; M15529; AAA42139.1; -;
 CC EMBL; M15528; -; NOT_ANNOTATED_CDS.
 CC PIR; A40147; RHRTG.

CC InterPro; IPR002012; GnRH.
 CC InterPro; IPR004079; GonadoliberinI.
 CC Pfam; PF00446; GnRH; 1.
 CC PRINTS; PR01541; GONADOLIBERNI.
 CC PROSITE; PS00473; GnRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Signal; Pyroglutamate carboxylic acid.

CC SIGNAL 1 23
 CC CHAIN 24 92
 CC PEPTIDE 24 92
 CC PEPTIDE 37 92
 CC ACT_SITE 26 26

CC MOD_RES 24 24
 CC MOD_RES 33 33
 CC SEQUENCE 92 AA; 10500 MW; 494B5C64DAB3EB3 CRC64;

Query Match 22.4%; Score 61.5; DB 1; Length 92;
 Best Local Similarity 51.7%; Pred. No. 0.62;
 Matches 15; Conservative 3; Mismatches 4; Indels 7; Gaps 2;

QY 28 VPKVSAS-----HLRG-PSLHWSYGLRP 49
 DB 4 IPKLMARVLLTVCLGSCSHWSYGLRP 32

RESULT 12
 GON1_TUPGB STANDARD; PRT; 92 AA.

AC Q95375;
 DT 13-DEC-1998 (Rel. 37, Created)
 DT 13-DEC-1998 (Rel. 37, Last sequence update)
 DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide II].
 GN GNRH1 OR GnRH.

OS Tupia glis belangeri (Common tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Scandentia; Tupaiidae; Tupaiia.
 OX NCBI_TaxID=37347;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=97079639; PubMed=8921350;

RA Kasten T.L., White S.A., Norton T.T., Bond C.T., Adelman J.P.,
 RA Fernald R.D.;
 RT "Characterization of two new proGnRH mRNAs in the tree shrew:
 RT first direct evidence for mesencephalic GnRH gene expression in a
 RT placental mammal.";
 RL Gen. Comp. Endocrinol. 104:7-19(1996).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.

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CC
 CC EMBL; U63326; AAB16837.1; -;
 CC InterPro; IPR002012; GnRH.
 CC InterPro; IPR004079; GonadoliberinI.
 CC Pfam; PF00446; GnRH; 1.
 CC PRINTS; PR01541; GONADOLIBERNI.
 CC PROSITE; PS00473; GnRH; 1.
 CC Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 CC Placenta; Signal; Pyroglutamate carboxylic acid.

CC SIGNAL 1 23
 CC CHAIN 24 92
 CC PEPTIDE 24 92
 CC PEPTIDE 37 92
 CC ACT_SITE 26 26

CC MOD_RES 24 24
 CC MOD_RES 33 33
 CC SEQUENCE 92 AA; 10197 MW; 4FDBF2C58CF5F63B CRC64;

Query Match 21.9%; Score 60; DB 1; Length 92;
 Best Local Similarity 52.4%; Pred. No. 0.95;
 Matches 11; Conservative 4; Mismatches 4; Indels 2; Gaps 1;

QY 2 HWSYGLRPGS--SGPSLENNF 20
 DB 25 HWSYGLRPGKRNALDSF 45

RESULT 13
 GON1_MACMU STANDARD; PRT; 67 AA.

AC P55247;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DE Progonadoliberin I precursor [Contains: Gonadoliberin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I); GnRH-associated peptide I]
 DE (Fragment).
 GN GNRH1 OR GnRH OR LHRH.

OS Macaca mulatta (Rhesus macaque).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
 OC Cercopithecinae; Macaca.
 OX NCBI_TaxID=9544;
 RN [1]

RP SEQUENCE FROM N.A.
 RC TISSUE=Hypothalamus;
 RX MEDLINE=95124501; PubMed=7545971;

RA Ma Y.J., Costa M.E., Ojeda S.R.;
 RA "Developmental expression of the genes encoding transforming growth
 RA factor alpha and its receptor in the hypothalamus of female thes
 RA macaques.";
 RL Neuroendocrinology 60:346-359(1994).

CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 CC the secretion of both luteinizing and follicle-stimulating
 CC hormones.

CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the GnRH family.

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CC EMBL; S75918; AAB33096.1; -;

DR PIR, I78541; I78541.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; GonadoliberinI.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GNADOLIBERNI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 FT SIGNAL 1 1
 FT CHAIN <1 5
 FT PEPTIDE 6 >67
 FT PEPTIDE 6 15
 FT ACT_SITE 19 >67
 FT ACT_SITE 8
 FT MOD_RES 6 6
 FT MOD_RES 15 15
 FT NON_TER 67
 FT SEQUENCE 67 AA; 7573 MW; 505394DAA261A3F2 CRC64;
 Query Match 21.5%; Score 59; DB 1; Length 67;
 Best Local Similarity 52.4%; Pred. No. 0.88;
 Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;
 QY 2 HWSYGLRPGS--SGPSLNFF 20
 DB 7 HWSYGLRPGKDAENLMSF 27
 RESULT 14
 ID GONI_HUMAN STANDARD; PRT; 92 AA.
 AC P01148;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DE Progonadoliberein I precursor (Contains: Gonadoliberin I (LH-RH I)
 DE (Luteinizing hormone-releasing hormone I) (Gonadotropin-releasing
 DE hormone I) (GnRH I) (Luliberin I) (Gonadorelin); GnRH-associated
 DE peptide I).
 GN GNRI1 OR GNRI1 OR LHRH.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89366682; PubMed=2671939;
 RA Hayflick J.S., Adelman J.P., Seeburg P.H.;
 RT "The complete nucleotide sequence of the human gonadotropin-releasing
 hormone gene.";
 RL Nucleic Acids Res. 17:6403-6403 (1989).
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86094338; PubMed=2867548;
 RA Adelman J.P., Mason A.J., Hayflick J.S., Seeburg P.H.;
 RT "Isolation of the gene and hypothalamic cDNA for the common precursor
 of gonadotropin-releasing hormone and prolactin release-inhibiting
 factor in human and rat.";
 RL Proc. Natl. Acad. Sci. U.S.A. 83:179-183 (1986).
 RP SEQUENCE FROM N.A. AND VARIANT SER-16.
 RX MEDLINE=85012739; PubMed=6090951;
 RA Seeburg P.H., Adelman J.P.;
 RT "Characterization of cDNA for precursor of human luteinizing hormone
 releasing hormone.";
 RL Nature 311:666-668 (1984).
 RP SEQUENCE OF 24-33.
 RX MEDLINE=83126573; PubMed=6760865;
 RA Tan L., Rousseau P.;

RT "The chemical identity of the immunoreactive LHRH-like peptide
 biosynthesized in the human placenta.";
 RL Biochem. Biophys. Res. Commun. 109:1061-1071 (1982).
 RN [5]
 RP VARIANT SER-16.
 RX MEDLINE=99318093; PubMed=10391209;
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RA "Characterization of single-nucleotide polymorphisms in coding regions
 of human genes.";
 RL Nat. Genet. 22:231-238 (1999).
 RN [6]
 RP ERRATUM.
 RA Cargill M., Altshuler D., Ireland J., Sklar P., Ardlie K., Patil N.,
 Shaw N., Lane C.R., Lim E.P., Kalyanaram N., Nemesh J., Ziaugra L.,
 Friedland L., Rolfe A., Warrington J., Lipshutz R., Daley G.Q.,
 Lander E.S.;
 RA Nat. Genet. 23:373-373 (1999).
 CC -!- FUNCTION: Stimulates the secretion of gonadotropins; it stimulates
 the secretion of both luteinizing and follicle-stimulating
 hormones.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- PHARMACEUTICAL: Available under the names Factrel (Ayerst Labs),
 Lutrepulse or Lutrelief (Perring Pharmaceuticals) and Relisorm
 (Serono).
 CC -!- SIMILARITY: Belongs to the GnRH family.
 CC
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 CC
 DR EMBL; X01059; CAA25526.1; -
 DR EMBL; M12578; AAA35916.1; -
 DR EMBL; X15215; CAA33285.1; -
 DR PIR; S05308; RHUG.
 DR Genew; HGNC:4419; GNRI1.
 DR MIM; 152760.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005183; F:lutinizing hormone-releasing factor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0008285; P:negative regulation of cell proliferation; TAS.
 DR GO; GO:0007165; P:signal transduction; TAS.
 DR InterPro; IPR002012; GnRH.
 DR InterPro; IPR004079; GonadoliberinI.
 DR Pfam; PF00446; GnRH; 1.
 DR PRINTS; PR01541; GNADOLIBERNI.
 DR PROSITE; PS00473; GnRH; 1.
 KW Cleavage on pair of basic residues; Hormone; Amidation; Hypothalamus;
 KW Placenta; Pharmaceutical; Signal; Polymorphism;
 KW Pyrrolidone carboxylic acid.
 FT SIGNAL 1 23
 FT CHAIN 24 92
 FT PEPTIDE 24 33
 FT PEPTIDE 37 92
 FT ACT_SITE 26 26
 FT MOD_RES 24 24
 FT MOD_RES 33 33
 FT VARIANT 16 16
 FT SEQUENCE 92 AA; 10380 MW; 30A72221B076FA79 CRC64;
 SQ
 Query Match 21.5%; Score 59; DB 1; Length 92;
 Best Local Similarity 52.4%; Pred. No. 1.3;
 Matches 11; Conservative 3; Mismatches 5; Indels 2; Gaps 1;

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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:54 ; Search time 49.4163 Seconds
(without alignment)
319.245 Million cell updates/sec

Title: US-09-848-834a-18
Perfect score: 274
Sequence: 1 XHWSXGLRFGSSGSLFNFN.....VSASHLEGPLHWSYGLRPX 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL 25:
1: sp.archaea.*
2: sp.bacteria.*
3: sp.fungi.*
4: sp.human.*
5: sp.invertebrate.*
6: sp.mammal.*
7: sp.mhc.*
8: sp.organelle.*
9: sp.phage.*
10: sp.plant.*
11: sp.rodent.*
12: sp.virus.*
13: sp.vertibrate.*
14: sp.unclassified.*
15: sp.rvirus.*
16: sp.bacteriap.*
17: sp.archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	114	41.6	451	Q91A13	Q91A13 clostridium
2	114	41.6	1310	Q93N27	Q93N27 clostridium
3	64	23.4	361	Q45848	Q45848 clostridium
4	64	23.4	361	Q45846	Q45846 clostridium
5	64	23.4	441	Q9X708	Q9X708 clostridium
6	64	23.4	1268	Q45851	Q45851 clostridium
7	64	23.4	1291	Q92AJ8	Q92AJ8 clostridium
8	64	23.4	1291	Q93G71	Q93G71 clostridium
9	64	23.4	1291	Q933K0	Q933K0 clostridium
10	64	23.4	1291	Q08077	Q08077 clostridium
11	64	23.4	1291	Q8GR96	Q8GR96 clostridium
12	64	23.4	2082	Q9ACR4	Q9ACR4 streptomyc
13	62.5	22.8	1291	Q93HT3	Q93HT3 clostridium
14	61.5	22.4	200	Q45YU6	Q45YU6 homo sapien
15	61	22.3	228	Q9J2H3	Q9J2H3 macaca mula
16	61	22.3	502	Q9X8T8	Q9X8T8 streptomyc

17	61	22.3	1278	2	Q57236	Q57236 clostridium
18	60.5	22.1	363	10	Q9FF71	Q9FF71 arabidopsis
19	59.5	21.7	657	10	Q9XE83	Q9XE83 sorghum bic
20	59.5	21.7	1285	2	Q45967	Q45967 clostridium
21	59.5	21.7	1285	2	Q9LBR1	Q9LBR1 clostridium
22	59.5	21.7	1999	16	Q8YWB9	Q8YWB9 anabaena sp
23	59	21.5	940	10	Q7XLI6	Q7XLI6 oryza sativ
24	58	21.2	91	13	Q9FRH0	Q9FRH0 anguilla ja
25	57.5	21.0	234	12	Q9W9A5	Q9W9A5 simian viru
26	57.5	21.0	234	12	Q92837	Q92837 simian viru
27	57.5	21.0	352	12	Q98VM1	Q98VM1 simian viru
28	57.5	21.0	352	12	Q9W9F7	Q9W9F7 simian viru
29	57.5	21.0	352	12	Q80FH1	Q80FH1 simian viru
30	57.5	21.0	352	12	Q91OV5	Q91OV5 simian viru
31	57.5	21.0	423	2	Q7WSQ9	Q7WSQ9 arthrobacte
32	57.5	21.0	426	2	Q8KN97	Q8KN97 pseudomonas
33	57.5	21.0	766	4	Q96ME8	Q96ME8 homo sapien
34	57.5	21.0	836	11	Q70595	Q70595 rattus norv
35	57.5	21.0	842	11	Q9DC29	Q9DC29 mus musculu
36	57.5	21.0	896	4	Q9HAQ7	Q9HAQ7 homo sapien
37	57	20.8	370	10	Q8W414	Q8W414 cucumis sat
38	57	20.8	430	2	Q9XAV1	Q9XAV1 pseudomonas
39	57	20.8	685	16	Q912G5	Q912G5 pseudomonas
40	57	20.8	866	5	Q9VF20	Q9VF20 pseudophila
41	57	20.8	1280	2	Q9ZAJ5	Q9ZAJ5 clostridium
42	56.5	20.6	94	13	Q8JFY3	Q8JFY3 oreochromis
43	56.5	20.6	98	13	Q805A5	Q805A5 oreochromis
44	56.5	20.6	113	2	Q9KW76	Q9KW76 staphylococ
45	56.5	20.6	140	2	Q9K2Q0	Q9K2Q0 staphylococ

ALIGNMENTS

RESULT 1
Q9LA13
ID Q9LA13 PRELIMINARY; PRT; 451 AA.
AC Q9LA13, 2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Tetanus toxin (Fragment).
OS Clostridium tetani.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1513;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=20886;
RA He H.J., Shi H.J., He Z.Y., Yuan Q.S., Wu X.F.;
RT "Fragment C of Tetanus Toxin".
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF154828; AAF73267.1; -.
DR HSP; P04958; IABD.
DR GO; GO:0004866; F:endoropeptidase inhibitor activity; IEA.
DR InterPro; IPR008985; ConA like lec_g1.
DR InterPro; IPR001064; Crystallin.
DR InterPro; IPR002160; Kunitz legume
DR PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 1.
FT NONTER
SQ SEQUENCE 451 AA; 51823 MW; 69A8C5F030E6CD8E CRC64;

Query Match 41.6%; Score 114; DB 2; Length 451;
Best Local Similarity 95.5%; Pred. No. 2.5e-06;
Matches 21; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 16 LFNNFTVSFWLRVPKVSASHLE 37
Db 82 MFNNFTVSFWLRVPKVSASHLE 103

RESULT 2
Q93N27

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SQ SEQUENCE 361 AA; 42131 MW; A2E0FFFC81F9553DD CRC64;

Query Match      23.4%; Score 64; DB 2; Length 361;
Best Local Similarity 62.5%; Pred. No. 5.5;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SLFNFTVSVFWLRVPK 30
DB 288 SMFLDFSVSFWIRPK 303
|.:.:|||:|.:.|
|.:.:|||:|.:.|

RESULT 4
Q45846 PRELIMINARY; PRT; 361 AA.
ID Q45846
AC Q45846;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Botulinum neurotoxin type B (fragment).
GN BONT/B.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
CX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=type B;
RX MEDLINE=84013372; PubMed=8408542;
RA Campbell K., East A.K., Collins M.D.;
RT "Gene probes for identification of the botulin neurotoxin gene and specific identification of neurotoxin types B, E, and F.";
RL J. Clin. Microbiol. 31:2255-2262(1993).
DR EMBl; X70814; CAA50145.1; -.
DR HSP; P10845; 3BTA.
DR GO; GO:0015070; F:Toxin activity; IEA.
DR InterPro; IPR009885; ConA_like_lec_gl.
KW Neurotoxin.
FT NON TER 1
FT NON TER 361
FT NON TER 1
SQ SEQUENCE 361 AA; 42175 MW; 533EA98735CD98E1 CRC64;

Query Match      23.4%; Score 64; DB 2; Length 361;
Best Local Similarity 62.5%; Pred. No. 5.5;
Matches 10; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 15 SLFNFTVSVFWLRVPK 30
DB 288 SMFLDFSVSFWIRPK 303
|.:.:|||:|.:.|
|.:.:|||:|.:.|

RESULT 5
Q9X708 PRELIMINARY; PRT; 441 AA.
ID Q9X708
AC Q9X708;
DT 01-NOV-1999 (TREMBlrel. 12, Created)
DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Botulinum neurotoxin type B (Fragment).
GN BONT/B.
OS Clostridium botulinum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
CX NCBI_TaxID=1491;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343691; PubMed=10413679;
RA Lalli G., Herreros J., Osborne S.I., Montecucco C., Rossetto O., Schiavo G.;
RT "Functional characterisation of tetanus and botulinum neurotoxins binding domains.";
RL J. Cell Sci. 112:2715-2724(1999).
DR EMBl; AJ242628; CAB43706.1; -.
DR HSP; P10845; 3BTA.
```

DT 01-MAY-1999 (TREMBlrel. 10, Created)

RESULT 10
Q08077
ID Q08077 PRELIMINARY; PRT; 1291 AA.
AC Q08077;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE BONT/B.
DE BONT/B.
OS Clostridium botulinum.

[illegible]

Db 114 HWPYHLWPG--GPSLWLRVSRRAIRGSLV-RNHSQQSQSMEDCG 155

RESULT 15

Q9J2H3 PRELIMINARY; PRT; 228 AA.
AC Q9J2H3; 2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE ORF014-L.
OS Macaca mulatta rhadinovirus 26-95.
OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Rhadinovirus.
OX NCBI_taxid=119193;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Macaca mulatta rhadinovirus isolate 26-95;
RX MEDLINE=20173730; PubMed=10708456;
RA Alexander L., Denekamp L., Knapp A., Auerbach M.R., Damania B.,
RA Desrosiers R.C.;
RT "The primary sequence of rhesus monkey rhadinovirus isolate 26-95:
RT sequence similarities to Kaposi's sarcoma-associated herpesvirus and
RT rhesus monkey rhadinovirus isolate 17577.";
RL J. Virol. 74:3388-3398(2000).
DR EMBL; AF210726; AAF60068.1; -.
SQ SEQUENCE 228 AA; 23930 MW; 62DF7341B48C83B6 CRC64;

Query Match 22.3%; Score 61; DB 12; Length 228;
Best Local Similarity 39.0%; Pred.No. 8;
Matches 16; Conservative 2; Mismatches 17; Indels 6; Gaps 1;

QY 9 PGSSGPSLNNFTVSWLRVPKYSASHLEGPSLHWSYGLRP 49
||| ||| : ||| : |||
Db 132 PGGGPQAEDNGTGTGFLPRVGTPTPSHL-----WPAGLCP 166

Search completed: March 10, 2004, 09:25:39
Job time : 50.4163 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 10, 2004, 08:58:48 ; Search time 75.2918 seconds
(without alignment)
187.635 Million cell updates/sec

Title: US-09-848-834A-18
Perfect score: 274
Sequence: 1 XHWSYGLRPGSGPSLFNFP.....VSASHLGGPSLHNSYGLRXP 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272	99.3	50	5	AAU11429 Synthetic
2	199	72.6	37	5	AAU11425 Synthetic
3	185	67.5	34	5	AAU11421 Synthetic
4	152	55.5	32	2	AAU1421 LHRH-cont
5	145	52.9	46	5	AAU1430 Synthetic
6	141.5	51.6	47	5	AAU1428 Synthetic
7	138.5	50.5	51	5	AAU1431 Synthetic
8	126	46.0	708	7	ABR82479 Modified
9	125	45.6	717	7	ABR82478 Modified
10	123	44.9	109	4	AB20150 Growth di
11	123	44.9	194	6	AAO30488 Human TNF
12	121.5	44.3	750	3	AAU1425 Synthetic
13	121	44.2	216	3	AAU1421 Synthetic
14	121	44.2	287	6	AAU1428 Synthetic
15	121	44.2	537	7	AAU1431 Synthetic
16	121	44.2	750	3	AAU1425 Synthetic
17	120.5	44.0	109	4	AB20150 Growth di
18	120	43.8	188	3	AAU1421 Synthetic
19	120	43.8	285	6	AAU1425 Synthetic
20	119.5	43.6	109	4	AB20150 Growth di
21	119.5	43.6	750	3	AAU1425 Synthetic
22	119	43.4	122	3	AAU1421 Synthetic
23	119	43.4	122	3	AAU1421 Synthetic
24	118.5	43.2	31	3	AAU1421 Synthetic
25	118.5	43.2	158	2	AAU1421 Synthetic

26	118.5	43.2	158	5	AB507282	Human TNF
27	118.5	43.2	693	3	AAU1425	Mutant hu
28	118.5	43.2	693	3	AAU1425	Mutant hu
29	118.5	43.2	750	3	AAU1425	Mutant hu
30	118.5	43.2	750	3	AAU1425	Mutant hu
31	118	43.1	158	5	AAU1425	Mutant hu
32	118	43.1	158	5	AAU1425	Mutant hu
33	118	43.1	703	3	AAU1425	Mutant hu
34	118	43.1	761	3	AAU1425	Mutant hu
35	117	42.7	124	3	AAU1425	Mutant hu
36	117	42.7	124	3	AAU1425	Mutant hu
37	117	42.7	160	4	AAU1425	Mutant hu
38	117	42.7	160	4	AAU1425	Mutant hu
39	117	42.7	514	6	AAU1425	Mutant hu
40	116	42.3	31	3	AAU1425	Mutant hu
41	116	42.3	43	4	AAU1425	Mutant hu
42	116	42.3	43	4	AAU1425	Mutant hu
43	116	42.3	72	4	AAU1425	Mutant hu
44	116	42.3	109	4	AAU1425	Mutant hu
45	116	42.3	136	4	AAU1425	Mutant hu

ALIGNMENTS

RESULT 1
AAU11429
ID AAU11429 standard; peptide; 50 AA.

AC AAU11429;

XX 12-MAR-2002 (first entry)

XX Synthetic immunogen peptide 10.

XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;

XX luteinising hormone releasing hormone; LHRH; contraceptive;

XX promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;

XX breast cancer; uterine cancer; gynaecological cancer; endometriosis;

XX uterine fibroid; benign prostatic hypertrophy; prostate cancer.

XX Clostridium tetani.

OS Mammalia.

OS Synthetic.

OS Chimeric.

XX Key Location/Qualifiers

FT Peptide 1. .10

FT Peptide /note= "Gonadotrophin releasing hormone epitope (1. .10 aa)"

FT Misc-difference 1

FT Peptide /label= OTHER

FT Peptide /note= "Other= Pyro-glutamic acid or 5-oxo proline"

FT Peptide /note= "Spacer peptide"

FT Peptide /note= "Tetanus toxoid (947-967 aa)"

FT Peptide /note= "Spacer peptide"

FT Peptide /note= "Gonadotrophin releasing hormone epitope (2-10 aa)"

FT Modified-site 50

FT Modified-site /note= "Amidated glycine or glycylamide"

XX WO200185763-A2.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US014363.

XX 05-MAY-2000; 2000US-0202328P.

PA (APHT-) APHTON CORP.
 XX Grimes S, Michaeli D, Stevens VC;
 XX WPI; 2002-049440/06.
 XX
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.
 XX
 XX Claim 11; Page 11; 43pp; English.
 XX
 XX The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX
 XX Sequence 50 AA;
 SQ
 Query Match 99.3%; Score 272; DB 5; Length 50;
 Best Local Similarity 100.0%; Pred. No. 1.6e-28;
 Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HWSYGLRPGSSGSLFNNFTVFWLRVVKVSASHLEGSLHWSYGLRP 49
 DB 2 HWSYGLRPGSSGSLFNNFTVFWLRVVKVSASHLEGSLHWSYGLRP 49
 RESULT 2
 AAU11425
 ID AAU11425 standard; peptide; 37 AA.
 XX
 XX AAU11425;
 AC
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Synthetic immunogen peptide 6.
 XX
 XX Gonadotropin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 XX Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1. .10
 FT Peptide /note= "Gonadotropin releasing hormone epitope"
 FT Misc-difference 1
 FT /label= OTHER
 FT /note= "Pyro-glutamic acid or 5-oxo proline"
 FT Peptide 11. .16
 FT /note= "Spacer peptide"
 FT Peptide 17. .37
 FT /note= "Tetanus toxoid sequence (947-967 aa)"
 XX
 XX WO200185763-A2.
 PN
 XX 15-NOV-2001.
 PD
 XX

PF 04-MAY-2001; 2001WO-US014363.
 XX
 XX 05-MAY-2000; 2000US-0202328P.
 XX
 XX (APHT-) APHTON CORP.
 PA
 XX Grimes S, Michaeli D, Stevens VC;
 PI
 XX WPI; 2002-049440/06.
 DR
 XX
 XX Novel synthetic immunogen for inducing immune response against
 PT gonadotropin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.
 XX
 XX Claim 11; Page 9; 43pp; English.
 PS
 XX The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotropin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone, LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX
 XX Sequence 37 AA;
 SQ
 Query Match 72.6%; Score 199; DB 5; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5.4e-19;
 Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 HWSYGLRPGSSGSLFNNFTVFWLRVVKVSASHLE 37
 DB 2 HWSYGLRPGSSGSLFNNFTVFWLRVVKVSASHLE 37
 RESULT 3
 AAU11421
 ID AAU11421 standard; peptide; 34 AA.
 XX
 XX AAU11421;
 AC
 XX
 DT 12-MAR-2002 (first entry)
 XX
 DE Synthetic immunogen peptide 2.
 XX
 XX Gonadotropin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 XX Clostridium tetani.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1. .21
 FT Peptide /note= "Tetanus toxoid sequence (947-967 aa)"
 FT Peptide 22. .25
 FT /note= "Spacer peptide"
 FT Peptide 26. .34
 FT /note= "Gonadotropin releasing hormone epitope"
 FT Modified-site 34
 FT /note= "Amidated glycine or glycine amide"
 XX
 XX WO200185763-A2.
 PN

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XX PD 15-NOV-2001.
XX PF 04-MAY-2001; 2001WO-US014363.
XX PF 05-MAY-2000; 2000US-0202328P.
XX PR (APHT-) APHTON CORP.
XX PA Grimes S, Michaeli D, Stevens VC;
XX PI WPI; 2002-049440/06.
XX DR Novel synthetic immunogen for inducing immune response against
XX DR Gonadotropin releasing hormone, comprises fusion peptide having
XX DR promiscuous helper T-cell peptide epitope and immunogenic peptide epitope
XX DR or its analog.
XX PS Claim 11; Page 7; 43pp; English.
XX CC The invention relates to a synthetic immunogen for inducing specific
XX CC antibodies against gonadotropin releasing hormone (GnRH) also known as
XX CC luteinising hormone releasing hormone, (LHRH) comprising a fusion peptide
XX CC which comprises a promiscuous helper T-cell peptide epitope and
XX CC immunogenic peptide epitope or its analogue. The synthetic immunogen is
XX CC useful inducing an immune response against GnRH in an animal subject, and
XX CC as such is useful as a contraceptive and in the treatment of diseases
XX CC such as cancer (of the breast, uterus and other gynaecological cancer),
XX CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
XX CC prostate cancer. The immunogen is effective in eliciting high and
XX CC specific anti-GnRH antibody titres. The present sequence is a synthetic
XX CC immunogen of the invention
XX SQ Sequence 34 AA;

Query Match 67.5%; Score 185; DB 5; Length 34;
Best Local Similarity 100.0%; Pred. NO. 3.5e-17; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 0;

QY 17 FNNFTVSPFLRPVKVSASHLEGPSLHWSYGLRP 49
DB 1 FNNFTVSPFLRPVKVSASHLEGPSLHWSYGLRP 33

RESULT 4
AAR62702
ID AAR62702 standard; peptide; 32 AA.
AC AAR62702;
XX 25-MAR-2003 (revised)
DT 10-SEP-1995 (first entry)
XX LHRH-containing immunogenic peptide.
DE Helper T cell epitope; universal immune stimulator; invasin; haptin;
KW vaccine; LHRH; luteinising hormone releasing hormone; prostate;
KW androgen-dependent carcinoma; antitumour; infertility; tetanus toxin.
XX Synthetic.
OS Key Location/Qualifiers
FH Domain 1..22
FT /note= "tetanus toxin helper T cell epitope"
FT Domain 23..32
FT /note= "LHRH haptin"
XX WO9425060-A1.
XX 10-NOV-1994.
XX 28-APR-1994; 94WO-US004832.

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PR 27-APR-1993; 93US-00057166.
XX 14-APR-1994; 94US-00229275.
XX (LADD/) LADD A E.
XX PA (WANG/) WANG C Y.
XX PA (ZAMB/) ZAMB T.
XX PI Ladd AE, Wang CY, Zamb T;
XX WPI; 1994-357910/44.
XX Immunogenic luteinising hormone releasing hormone peptide(s) - that
XX suppress LHRH activity in males and females.
XX Claim 8; Page 84; 213pp; English.
XX CC Synthetic immunogenic peptides are provided in which a universal immune
XX CC stimulator is linked to a peptide or protein haptin containing B cell
XX CC and/or cytotoxic T lymphocyte epitopes, giving a product which causes
XX CC potent immune responses to the coupled peptide or protein. The stimulator
XX CC consists of (A) a promiscuous helper T cell epitope (Th) which elicits an
XX CC immune response to the coupled peptide in members of a heterogeneous
XX CC population expressing diverse HLA phenotypes, and (B) an adjuvant peptide
XX CC sequence from the invasin protein of Yersinia. Spacer amino acid
XX CC sequences (e.g. Gly-Gly) can be provided between the invasin and Th
XX CC domains and between the immune stimulator and haptin components. When the
XX CC haptin is LHRH, then optionally the invasin domain can be omitted from
XX CC the immune stimulator component. The present sequence represents an LHRH-
XX CC containing, invasin-free immunogenic peptide as above which can be used
XX CC as a potent vaccine for treating e.g. prostatic hyperplasia, androgen-
XX CC dependent carcinoma, prostatic carcinoma, recurrent functional ovarian
XX CC endometriosis, benign uterine tumours, recurrent functional ovarian
XX CC cysts, (severe) premenstrual syndrome or oestrogen-dependent breast
XX CC cancer, or for induction of infertility. (Updated on 25-MAR-2003 to
XX CC correct FN field.)
XX SQ Sequence 32 AA;

Query Match 55.5%; Score 152; DB 2; Length 32;
Best Local Similarity 87.9%; Pred. NO. 7.9e-13;
Matches 29; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 17 FNNFTVSPFLRPVKVSASHLEGPSLHWSYGLRP 49
DB 3 FNNFTVSPFLRPVKVSASHLE----HWSYGLRP 31

RESULT 5
AAU11430
ID AAU11430 standard; peptide; 46 AA.
XX AC AAU11430;
XX 12-MAR-2002 (first entry)
XX Synthetic immunogen peptide 11.
DE Gonadotropin releasing hormone; GnRH; synthetic immunogen;
XX luteinising hormone releasing hormone; LHRH; contraceptive;
XX promiscuous helper T-cell peptide epitope; immunogenic peptide epitope;
XX breast cancer; uterine cancer; gynaecological cancer; endometriosis;
XX uterine fibroid; benign prostatic hypertrophy; prostate cancer.
XX Clostridium tetani.
OS Mammalia.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FH Peptide 1..10
FT /note= "Gonadotropin releasing hormone epitope (1..10
FT aa)"
FT Misc-difference 1

```

Key	Location/Qualifiers
1..10	/note= "Gonadotrophin releasing hormone epitope (1..10 aa)"
Misc-difference 1	/label= OTHER
Peptide	/note= "Other= Pyro-glutamic acid or 5-oxo proline"
11..16	/note= "Spacer peptide"
17..34	/note= "Malaria CSP protein (288-302 aa)"
35..38	/note= "Spacer peptide"
39..47	/note= "Gonadotrophin releasing hormone epitope (2-10 aa)"
Modified-site 47	/note= "Amidated glycine or glycinamide"
WC200185763-A2.	
15-NOV-2001.	
04-MAY-2001; 2001WO-US014363.	
05-MAY-2000; 2000US-0202328P.	
(APHT-) APHTON CORP.	
Grimes S, Michaeli D, Stevens VC;	
WPI; 2002-049440/06.	
Novel synthetic immunogen for inducing immune response against gonadotropin releasing hormone, comprises fusion peptide having promiscuous helper T-cell peptide epitope and immunomimic peptide epitope or its analog.	
Claim 11; Page 11; 43pp; English.	
The invention relates to a synthetic immunogen for inducing specific antibodies against gonadotropin releasing hormone (GnRH) also known as luteinising hormone releasing hormone, LH(RH) comprising a fusion peptide which comprises a promiscuous helper T-cell peptide epitope and an immunomimic peptide epitope or its analogue. The synthetic immunogen is useful inducing an immune response against GnRH in an animal subject, and as such is useful as a contraceptive and in the treatment of diseases such as cancer (of the breast, uterus and other gynaecological cancer), endometriosis, uterine fibroids, benign prostatic hypertrophy and prostate cancer. The immunogen is effective in eliciting high and specific anti-GnRH antibody titres. The present sequence is a synthetic immunogen of the invention	
Sequence 47 AA;	
Query Match	51.6%; Score 141.5; DB 5; Length 47;
Best Local Similarity	58.8%; Pred. No. 3.1e-11;
Matches 30; Conservative 1; Mismatches 11; Indels 9; Gaps 2	
Qy	2 HWSYGLRPGSSGSPSLFNNFTVSFWLVRPKVSASHL---EGPSLHWSYGLRP 49
Db	2 HWSYGLRPGSSGSPSL-----KLSEIKGVIVHRLEGVGSPSLHWSYGLRP 46
RESULT 7	
AAU11431	

ID XX AAU11431 standard; peptide; 51 AA.
 AC AAU11431;
 XX 12-MAR-2002 (first entry)
 DT Synthetic immunogen peptide 12.
 DE
 XX Gonadotrophin releasing hormone; GnRH; synthetic immunogen;
 KW luteinising hormone releasing hormone; LHRH; contraceptive;
 KW promiscuous helper T-cell peptide epitope; immunomimic peptide epitope;
 KW breast cancer; uterine cancer; gynaecological cancer; endometriosis;
 KW uterine fibroid; benign prostatic hypertrophy; prostate cancer.
 XX
 OS Plasmodium falciparum.
 OS Mammalia.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..10
 FT /note= "Gonadotrophin releasing hormone epitope (1..10 aa)"
 FT Misc-difference 1
 FT /label= OTHER
 FT /note= "Pyro-glutamic acid or 5-oxo proline"
 FT Peptide 11..16
 FT /note= "Spacer peptide"
 FT Peptide 17..36
 FT /note= "Malaria CSP protein (378-398 aa)"
 FT Peptide 37..42
 FT /note= "Spacer peptide"
 FT Peptide 43..51
 FT /note= "Gonadotrophin releasing hormone epitope (2-10 aa)"
 FT Modified-site 51
 FT /note= "Amidated glycine or glycineamide"
 XX
 PN WO200185763-A2.
 XX 15-NOV-2001.
 PD
 XX 04-MAY-2001; 2001WO-US014363.
 XX 05-MAY-2000; 2000US-0202328P.
 XX (APHT-) APHTON CORP.
 PA Grimes S, Michaeli D, Stevens VC;
 XX WPI; 2002-049440/06.
 XX
 PT Novel synthetic immunogen for inducing immune response against
 PT gonadotrophin releasing hormone, comprises fusion peptide having
 PT promiscuous helper T-cell peptide epitope and immunomimic peptide epitope
 PT or its analog.
 XX
 PS Claim 11; Page 12-13; 43pp; English.
 CC The invention relates to a synthetic immunogen for inducing specific
 CC antibodies against gonadotrophin releasing hormone (GnRH) also known as
 CC luteinising hormone releasing hormone (LHRH) comprising a fusion peptide
 CC which comprises a promiscuous helper T-cell peptide epitope and
 CC immunomimic peptide epitope or its analogue. The synthetic immunogen is
 CC useful inducing an immune response against GnRH in an animal subject, and
 CC as such is useful as a contraceptive and in the treatment of diseases
 CC such as cancer (of the breast, uterus and other gynaecological cancer),
 CC endometriosis, uterine fibroids, benign prostatic hypertrophy and
 CC prostate cancer. The immunogen is effective in eliciting high and
 CC specific anti-GnRH antibody titres. The present sequence is a synthetic
 CC immunogen of the invention
 XX
 SQ Sequence 51 AA;
 QY 11 SSGPS-----LFNNFTVSFMLRVPKVSASHLEGPSLH 42
 Query Match 46.0%; Score 136; DB 7; Length 708;
 Best Local Similarity 58.4%; Pred. No. 8.4e-08;
 Matches 26; Conservative 2; Mismatches 4; Indels 6; Gaps 1;
 Query Match 50.5%; Score 138.5; DB 5; Length 51;
 Best Local Similarity 54.7%; Pred. No. 8.4e-11;
 Matches 29; Conservative 4; Mismatches 11; Indels 9; Gaps 2;
 QY 2 HWSYGLRPGSGPSLFNNFTVSFMLRVPKVA-----SHLEGPSLHWSYGLRP 49
 DB 2 HWSYGLRPGSGPSLDEKIA-----KMEKASSVFNVNVSNGPSLHWSYGLRP 50
 RESULT 8
 ABR82479
 ID ABR82479 standard; protein; 708 AA.
 XX ABR82479;
 XX 20-NOV-2003 (first entry)
 DT Modified human CEA-TT P2 and P30 epitopes.
 DE
 XX CEA; immune response; carcinoembryonic antigen; antigen presenting cell;
 KW APC; cytostatic; vaccine; human; tetanus toxoid; p2; p30; antigen.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..34
 FT /note= "signal peptide"
 FT Protein 35..708
 FT /note= "mature protein"
 XX
 PN WO2003059379-A2.
 XX 24-JUL-2003.
 PD
 XX 17-JAN-2003; 2003WO-DK000031.
 XX 17-JAN-2002; 2002DK-00000082.
 PR 17-JAN-2002; 2002US-0350047F.
 XX (PHAR-) PHARMEXA AS.
 PA Klysner S, Voldborg B;
 XX WPI; 2003-587260/55.
 DR N-PSDB; ACP35966.
 XX
 PT Inducing an immune response in humans against autologous carcinoembryonic
 PT antigen (CEA) comprises administering a modified CEA polypeptide, a
 PT nucleic acid encoding the polypeptide, or a microorganism expressing the
 PT polypeptide.
 XX
 PS Disclosure; Page 121-124; 140pp; English.
 CC The invention relates to inducing an immune response against autologous
 CC carcinoembryonic antigen (CEA) in an animal, e.g. human. The method
 CC involves effecting uptake and processing by antigen presenting cells
 CC (APCs) in the animal of at least 1 modified CEA polypeptide or of a
 CC nucleic acid encoding the modified CEA polypeptide or of a microorganism
 CC or virus expressing the modified CEA polypeptide to induce a CTL response
 CC and an antibody response that targets the autologous CEA. The method is
 CC useful in immunizing actively against diseases characterized by cells
 CC that express CEA. The present sequence represents a modified human CEA
 CC polypeptide that has tetanus toxoid (TT) P2 and P30 epitopes introduced
 CC in its sequence
 XX
 SQ Sequence 708 AA;
 QY 11 SSGPS-----LFNNFTVSFMLRVPKVSASHLEGPSLH 42
 Query Match 46.0%; Score 136; DB 7; Length 708;
 Best Local Similarity 58.4%; Pred. No. 8.4e-08;
 Matches 26; Conservative 2; Mismatches 4; Indels 6; Gaps 1;

Db 630 ASNPSPQYSWRIFNFTVSWLRVPKVSASHLEIPQOH 667

RESULT 9

ABR82478
ID ABR82478 standard; protein; 717 AA.

XX ABR82478;

XX 20-NOV-2003 (first entry)

DE Modified human CEA-TT P2 and P30 epitopes.

XX CEA; immune response; carcinoembryonic antigen; antigen presenting cell;
KW APC; cytostatic; vaccine; human; tetanus toxoid; P2; P30; antigen.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..34 "signal peptide"

FT Protein 35..717

FT /note= "mature protein"

XX WO2003059379-A2.

XX 24-JUL-2003.

XX 17-JAN-2003; 2003WO-DK000031.

XX 17-JAN-2002; 2002DK-00000082.

XX 17-JAN-2002; 2002US-0350047P.

XX (PHAR-) PHARMEXA AS.

XX Klysner S, Voldborg B;

XX WPI; 2003-587260/55.

XX N-PSDB; ACF35964.

XX Inducing an immune response in humans against autologous carcinoembryonic
PT antigen (CEA) comprises administering a modified CEA polypeptide, a
PT nucleic acid encoding the polypeptide, or a microorganism expressing the
PT polypeptide.

PS Disclosure; Page 114-117; 140pp; English.

XX The invention relates to inducing an immune response against autologous
CC carcinoembryonic antigen (CEA) in an animal, e.g. human. The method
CC involves effecting uptake and processing by antigen presenting cells
CC (APCs) in the animal of at least 1 modified CEA polypeptide or of a
CC nucleic acid encoding the modified CEA polypeptide, or of a microorganism
CC or virus expressing the modified CEA polypeptide to induce a CTL response
CC and an antibody response that targets the autologous CEA. The method is
CC useful in immunizing actively against diseases characterized by cells
CC that express CEA. The present sequence represents a modified human CEA
CC polypeptide that has tetanus toxoid (Tt) P2 and P30 epitopes introduced
CC in its sequence

XX Sequence 717 AA;

Query Match 45.6%; Score 125; DB 7; Length 717;

Best Local Similarity 96.0%; Pred. No. 1.2e-07;

Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 16 LFNNFTVSWLRVPKVSASHLEGPS 40

Db 692 LFNNFTVSWLRVPKVSASHLEGPS 716

RESULT 10

AAB20150

ID XX AAB20150 standard; protein; 109 AA.
AC XX AAB20150;
XX 30-APR-2001 (first entry)
XX Growth differentiation factor 8 AutoVac construct GDF-8 P30-3A.
DE Growth differentiation factor 8; GDF-8; myostatin; tetanus toxin;
KW T-cell epitope; down-regulation; vaccine; muscle; meat; cachexia;
KW cardiant; human; mutant; mutein.
XX Homo sapiens.
OS Clostridium tetani.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
FH Region 1..78
FT /note= "identical to residues 267-345 of human GDF-8"
FT Misc-difference 73
FT /note= "Cys-73 may be substituted by Ser to avoid
FT disulfide bond formation"
FT Region 79..109
FT /note= "tetanus toxoid P2 epitope"
FT Misc-difference 90..91
FT /note= "optionally replaced by Glu-Gly"
FT Region 100..109
FT /note= "identical to residues 366-375 of human GDF-8"
XX WO200105820-A2.
XX 25-JAN-2001.
XX 20-JUL-2000; 2000WO-DK000413.
XX 20-JUL-1999; 99DK-00001014.
XX 26-JUL-1999; 99US-0145275P.
XX (MEBI-) M & E BIOTECH AS.
XX Halkier T, Mouritsen S, Klysner S;
XX WPI; 2001-112680/12.
XX Increasing the muscle mass of animals used in meat production by down
PT regulating growth differentiation factor 8 (GDF-8) activity in the animal
PT through induction of anti-GDF-8 antibody production.

XX Example 1; Page 102-103; 110pp; English.

XX The present sequence is that of AutoVac construct GDF-8 P30-3A,
CC comprising the 109 C-terminal amino acid residues of human growth
CC differentiation factor 8 (GDF-8) in which residues 79-99 are replaced by
CC the promiscuous tetanus toxin T-cell epitope P30 (see AAB20144). It is an
CC object of the invention to produce a recombinant therapeutic vaccine that
CC is capable of effecting down-regulation of GDF-8 in order to increase the
CC muscle growth rate of farm animals. The vaccines (see AAB20145-53) are
CC capable of breaking autotolerance against autologous GDF-8. They comprise
CC the C-terminal portion of human GDF-8 in which a portion of the native
CC sequence is replaced by a T-cell epitope such as P30, with minimal
CC disturbance of the authentic 3-dimensional structure of the protein.
CC Nucleic acids encoding the GDF-8 variants can be used for genetic
CC immunization of the animals. Down-regulation of GDF-8 activity can
CC increase muscle mass by up to at least 45% in cattle, pigs and poultry
CC used for meat production, reducing the need for antibiotic feed-
CC additives. Anti-GDF8 vaccines can be used to treat human diseases such as
CC cancer cachexia where muscle atrophy is pronounced and for patients
CC suffering from acute and chronic heart failure

XX Sequence 109 AA;

Query Match 44.9%; Score 123; DB 4; Length 109;

```
Best Local Similarity 78.1%; Pred. No. 2.3e-08;
Matches 25; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 10 GSSG----PSLFNNFTVSFWLRVVKVSASHLE 37
   |||:|||||:|||||:|||||:|||||:
Db 68 GSAGPCCTPTKFNFTVSFWLRVVKVSASHLE 99

RESULT 11
AAO30488
ID AAO30488 standard; protein; 194 AA.
XX
AC AAO30488;
XX
DT 22-SEP-2003 (first entry)
XX
DE Human TNFalpha variant, TNF34-P2-P30.
XX
KW Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease;
KW tumour necrosis factor alpha; gene therapy; arthritis; human; mutant;
KW mutein; variant; tetanus toxoid; epitope.
XX
OS Homo sapiens.
OS Unidentified.
OS Chimeric.
XX
FH Key Location/Qualifiers
FT Region 2..109
FT /note= "Human TNF"
FT Region 110..124
FT /note= "Tetanus toxoid P2 epitope"
FT Region 125..145
FT /note= "Tetanus toxoid P30 epitope"
FT Region 146..194
FT /note= "Human TNF"
XX
PN WO2003042244-A2.
XX
PD 22-MAY-2003.
XX
PF 15-NOV-2002; 2002WO-DK000764.
XX
PR 16-NOV-2001; 2001DK-00001702.
XX
PR 16-NOV-2001; 2001US-0331575P.
XX
PA (PHAR-) PHARMEXA AS.
PA (KLYS/) KLYSNER S.
PA (NIEL/) NIELSEN F S.
PA (BRAT/) BRATT T.
PA (VOLD/) VOLDORF B.
PA (MOUR/) MOURITSEN S.
XX
PI Klyner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;
XX
DR WPI; 2003-449558/42.
XX
PT New immunogenic analogue of a polymeric protein, useful for preparing a
PT composition for treating inflammatory diseases e.g. arthritis.
XX
PS Claim 23; Page 158; 196pp; English.
XX
CC The invention relates to immunogenic analogues of multimeric proteins
CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis
CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic
CC analogues. The immunogenic analogue is useful for preparing a composition
CC for treating inflammatory diseases, e.g., arthritis. It is also used in
CC gene therapy. The present sequence is human TNFalpha variant protein with
CC an inserted tetanus toxoid P2 and P30 epitopes. This sequence is used to
CC illustrate the method of the invention
XX
SQ Sequence 194 AA;
Query Match 44.9%; Score 123; DB 6; Length 194;

Best Local Similarity 82.1%; Pred. No. 4.6e-08;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 16 LFNFTVSFWLRVVKVSASHLEGP SLHW 43
   |||:|||||:|||||:|||||:
Db 124 LFNFTVSFWLRVVKVSASHLEAEAKPW 151

RESULT 12
AA92633
ID AAY92633 standard; protein; 750 AA.
XX
AC AAY92633;
XX
DT 10-AUG-2000 (first entry)
XX
DE Mutant human prostate specific membrane antigen construct, hPSM1.10.
XX
KW Prostate specific membrane antigen; immunogenized construct; mutant;
KW vaccination; cytotoxic T-lymphocyte immunity; breast cancer;
KW prostate cancer; cell-associated peptide antigen; foreign epitope.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 24..38
FT /label= P2
FT /note= "foreign epitope"
FT Peptide 673..693
FT /label= P30
FT /note= "foreign epitope"
XX
PN WO200020027-A2.
XX
PD 13-APR-2000.
XX
PF 05-OCT-1999; 99WO-DK000525.
XX
PR 05-OCT-1998; 98DK-00001261.
XX
PR 20-OCT-1998; 98US-0105011P.
XX
PA (MEBI-) M & E BIOTECH AS.
XX
PI Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;
PI Gautam A, Birk P, Karlsson G;
XX
DR WPI; 2000-349917/30.
XX
PT Inducing immune responses to weakly immunogenic, tumor associated peptide
PT antigens for the treatment of breast and prostate cancer.
XX
PS Example 1; Page; 220pp; English.
XX
CC AAY92627-49 are mutant immunogenized human prostate specific membrane
CC antigen (PSM) constructs, which contain foreign epitopes (P2 and/or P30).
CC The immunogenic analogues of PSM can be used in the claimed method as an
CC autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody
CC binding regions and cysteine residues involved in disulfide bonds are
CC preserved in the immunogenized forms. The method is used for inducing
CC immune responses against weakly immunogenic cell-associated peptide
CC antigens (PA) such as those associated with cancers (self-proteins), e.g.
CC human prostate specific membrane antigen (PSM), heregulin 2 (Her2) and/or
CC fibroblast growth factor 8b (FGF8b). The method comprises effecting
CC simultaneous presentation by antigen producing cells (APCs) of the
CC animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte)
CC group derived from the PA and/or at least 1 B-cell group derived from the
CC cell-associated PA; and (2) at least 1 first T helper cell group which is
CC foreign to the animal. Analogues of human PSM, human Her2 and
CC human/murine FGF8b comprising a substantial part of all known and
CC predicted CTL and B-cell epitopes of the respective PA and including at
CC least one foreign T helper epitope are also claimed. The method is used
CC to treat prostate, prostate/breast or breast cancer when the PA is human
```

CC PSM, FGF8b and Her2, respectively. Note: This sequence was constructed from the wild type human PSM (AA92619), which appears on pages 184-187 of the specification

XX Sequence 750 AA;

Query Match 44.3%; Score 121.5; DB 3; Length 750;

Best Local Similarity 86.2%; Pred. No. 3.5e-07; Indels 1; Gaps 1; Mismatches 25; Conservative 0;

Qy 17 FNNFTVFWLRVFKVSASHLEGPSSLSWSY 45

Db 673 FNNFTVFWLRVFKVSASHLE-PSSHNY 700

RESULT 13

ID AA92665 standard; peptide; 216 AA.

XX AC AA92665;

XX 10-AUG-2000 (first entry)

XX MUC-1 analogue containing foreign epitopes.

XX Mucin repeat; MUC-1 analogue; vaccination; self-protein; cancer; cytotoxic T-lymphocyte immunity; breast cancer; prostate cancer; cell-associated peptide antigen; foreign epitope.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Peptide 61..75

FT /label= P2

FT Peptide 136..156

FT /label= P30

FT /note= "q"

XX WO200020027-A2.

XX 13-APR-2000.

XX 05-OCT-1999; 99WO-DK000525.

XX 05-OCT-1998; 98DK-00001261.

XX 20-OCT-1998; 98US-0105011P.

XX (MEBI-) M & E BIOTECH AS.

XX Steinaa L, Mouritsen S, Nielsen KG, Haaning J, Leach D, Dalum I;

PI Gautam A, Birk P, Karlsson G;

XX WPI; 2000-349917/30.

XX Inducing immune responses to weakly immunogenic, tumor associated peptide antigens for the treatment of breast and prostate cancer.

XX Example 4; Page; 220pp; English.

XX This is an immunogenized MUC-1 analogue containing foreign epitopes P2 and P30. Immunogenic analogues of MUC-1 and, e.g. human prostate specific membrane antigen (hPSM) can be used in the claimed method as an autovaccine to induce a CTL response. Subdominant CTL epitopes, antibody binding regions and cysteine residues involved in disulfide bonds are preserved in the immunogenized forms (see features table). 10 regions suitable for the insertion of foreign T helper epitopes were identified. The method is used for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (self-proteins), e.g. hPSM, heregulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCs) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the

CC cell-associated PA; and (2) at least 1 first T helper cell group which is foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope are also claimed. The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively. Note: This sequence does not appear in the specification. It was made using the mucin repeat sequence (AA92664), P2 and P30 (AA92625-26), which appear on pages 220, 213 and 214 respectively, of the specification

XX Sequence 216 AA;

Query Match 44.2%; Score 121; DB 3; Length 216;

Best Local Similarity 64.1%; Pred. No. 9.6e-08; Indels 10; Gaps 1; Mismatches 25; Conservative 2; Mismatches 2;

Qy 9 PGSSGP-----SLFNNFTVFWLRVFKVSASHLE 37

Db 118 PGSTAPPAGVTSAPDTRFNNFTVFWLRVFKVSASHLE 156

RESULT 14

ID AAO30459 standard; protein; 287 AA.

XX AC AAO30459;

XX 22-SEP-2003 (first entry)

XX hIL5.36 variant protein.

XX Multimeric protein; interleukin 5; IL5; TNFalpha; inflammatory disease; tumour necrosis factor alpha; gene therapy; arthritis; interleukin 5; IL5; epitope; human; tetanus toxoid; chimeric; variant; mutant; mutein.

XX Homo sapiens.

XX Unidentified.

XX Chimeric.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /note= "Human IL5 leader peptide"

FT Protein 20..287

FT /note= "Mature hIL5.36 protein"

FT Region 24..44

FT /note= "Tetanus toxoid P30 epitope"

FT Region 273..287

FT /note= "Tetanus toxoid P2 epitope"

XX WO2003042244-A2.

XX 22-MAY-2003.

XX 15-NOV-2002; 2002WO-DK000764.

XX 16-NOV-2001; 2001DK-00001702.

XX 16-NOV-2001; 2001US-0331575P.

XX (PHAR-) PHARMEXA AS.

XX (KLYS-) KLYSNER S.

XX (NIEL-) NIELSEN F S.

XX (BRAT-) BRATT T.

XX (VOLD-) VOLDBOG B.

XX (MOUR-) MOURITSEN S.

XX Klysner S, Nielsen FS, Bratt T, Voldborg B, Mouritsen S;

XX WPI; 2003-449558/42.

XX N-PSDB; AAL61295.

XX New immunogenic analogue of a polymeric protein, useful for preparing a composition for treating inflammatory diseases e.g. arthritis.

XX PS Claim 20; Page 115-117; 196pp; English.

XX CC The invention relates to immunogenic analogues of multimeric proteins

XX CC such as immunogenic variants of interleukin 5 (IL5) and tumour necrosis

XX CC factor alpha (TNF, TNFalpha) and methods for production of immunogenic

XX CC analogues. The immunogenic analogue is useful for preparing a composition

XX CC for treating inflammatory diseases, e.g., arthritis. It is also used in

XX CC gene therapy. The present sequence is a fusion construct variant which

XX CC comprises 2 human interleukin 5 (IL5) monomers joined by diglycine linker

XX CC and including terminally positioned tetanus toxoid epitopes P30 and P2.

XX CC This sequence is used to illustrate the method of the invention

XX SQ Sequence 287 AA;

Query Match 44.2%; Score 121; DB 6; Length 287;

Best Local Similarity 85.2%; Pred. No. 1.3e-07;

Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 14 PSLFNNFTVSWLRVPKVSASHLEGPS 40

DB 21 PTEFNNFTVSEWLRVPKVSASHLEIPT 47

RESULT 15

ABR82481

ID ABR82481 standard; protein; 537 AA.

XX AC ABR82481;

XX DT 20-NOV-2003 (first entry)

XX DE Truncated human CEA-TT P2 and P30 epitopes.

XX KW CEA; immune response; carcinoembryonic antigen; antigen presenting cell;

XX KW APC; cytostatic; vaccine; human; tetanus toxoid; P2; P30; antigen.

XX OS Synthetic.

XX FH Key Location/Qualifiers

FT Peptide 1..34

FT Protein /note= "signal peptide"

FT Protein 35..537

FT Protein /note= "mature protein"

XX PN WO2003059379-A2.

XX PD 24-JUL-2003.

XX PF 17-JAN-2003; 2003WO-DK0000031.

XX PR 17-JAN-2002; 2002DK-00000082.

XX PR 17-JAN-2002; 2002US-0350047P.

XX PA (PHAR-) PHARMEXA AS.

XX PI Klysner S, Voldborg B;

XX DR WPI; 2003-587260/55.

XX DR N-PSDB; ACF35968.

XX PT Inducing an immune response in humans against autologous carcinoembryonic

XX PT antigen (CEA) comprises administering a modified CEA polypeptide, a

XX PT nucleic acid encoding the polypeptide, or a microorganism expressing the

XX PT polypeptide.

XX PS Disclosure; Page 134-137; 140pp; English.

XX CC The invention relates to inducing an immune response against autologous

XX CC carcinoembryonic antigen (CEA) in an animal, e.g. human. The method

XX CC involves effecting uptake and processing by antigen presenting cells

XX CC (APCs) in the animal of at least 1 modified CEA polypeptide or of a

XX CC nucleic acid encoding the modified CEA polypeptide or of a microorganism

or virus expressing the modified CEA polypeptide to induce a CTL response

and an antibody response that targets the autologous CEA. The method is

useful in immunizing actively against diseases characterized by cells

that express CEA. The present sequence represents a truncated human CEA

polypeptide that has tetanus toxoid (TT) P2 and P30 epitopes introduced

in its sequence

XX SQ Sequence 537 AA;

Query Match 44.2%; Score 121; DB 7; Length 537;

Best Local Similarity 95.8%; Pred. No. 2.8e-07;

Matches 23; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 17 FNNFTVSEWLRVPKVSASHLEGPS 40

DB 513 FNNFTVSEWLRVPKVSASHLEGTS 536

Search completed: March 10, 2004, 09:12:13

Job time : 75.2918 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 10, 2004, 09:16:59 ; Search time 39.2996 Seconds
(without alignments)
268.645 Million cell updates/sec

Title: US-09-848-834A-18
Perfect score: 274
Sequence: 1 XHWSYGLRPGSSGSLFNNF.....VSASHLEGPLSHWSYGLRFX 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 809742 seqs, 211153259 residues

Total number of hits satisfying chosen parameters: 809742

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/FCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/FCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	99.3	50	9	US-09-848-834A-18
2	199	72.6	37	9	US-09-848-834A-18
3	185	67.5	34	9	US-09-848-834A-18
4	145	52.9	46	9	US-09-848-834A-18
5	141.5	51.6	47	9	US-09-848-834A-17
6	138.5	50.5	51	9	US-09-848-834A-20
7	123	44.9	194	14	US-10-295-074-46
8	121	44.2	287	14	US-10-295-074-13
9	120	43.8	285	14	US-10-295-074-11
10	118.5	43.2	158	14	US-10-297-942-18
11	118	43.1	158	14	US-10-297-942-12
12	117	42.7	514	14	US-10-295-074-59
13	116	42.3	158	14	US-10-297-942-2
14	115	42.0	194	14	US-10-295-074-47
15	114	41.6	158	14	US-10-297-942-10

Sequence 180, App
Sequence 183, App
Sequence 185, App
Sequence 186, App
Sequence 184, App
Sequence 2, Appli
Sequence 182, App
Sequence 181, App
Sequence 177, Appl
Sequence 11, Appl
Sequence 9, Appli
Sequence 3, Appli
Sequence 5, Appli
Sequence 17, Appl
Sequence 16, Appl
Sequence 149, App
Sequence 141, App
Sequence 145, App
Sequence 3, Appli
Sequence 4, Appli
Sequence 6, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 3, Appli
Sequence 8, Appli
Sequence 5, Appli
Sequence 5, Appli
Sequence 8, Appli
Sequence 28, Appli

US-10-452-024-180
US-10-452-024-183
US-10-452-024-185
US-10-452-024-186
US-10-452-024-184
US-09-816-467-2
US-10-452-024-182
US-10-452-024-181
US-10-452-024-177
US-10-130-973A-11
US-10-130-973A-9
US-10-130-973A-3
US-10-130-973A-5
US-10-130-973A-17
US-10-130-973A-16
US-10-452-024-149
US-10-241-596-141
US-10-452-024-145
US-09-943-548-3
US-09-848-834A-4
US-09-785-215-6
US-09-405-986-2
US-10-204-362-6
US-10-339-522-3
US-10-223-711-8
US-10-233-809A-6
US-10-261-208-5
US-10-295-074-5
US-10-372-111-8
US-10-411-544-28

ALIGNMENTS

RESULT 1

US-09-848-834A-18
; Sequence 16, Application US/09848834A
; Patent No. US20020078416A1
; GENERAL INFORMATION:
; APPLICANT: Aphton Corporation
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047
; CURRENT APPLICATION NUMBER: US/09/848,834A
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 18
; LENGTH: 50
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of huma
; OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 947-967 of the 1
; OTHER INFORMATION: anus toxoid precursor (Tentoxylisin) protein linked by a spacer
; OTHER INFORMATION: o amino acid sequence 2-10 of human GnRH
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
; NAME/KEY: MOD RES
; LOCATION: (50)..(50)
; OTHER INFORMATION: Amidated glycine or glycineamide
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(10)
; OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
; NAME/KEY: PEPTIDE
; LOCATION: (11)..(16)
; OTHER INFORMATION: Spacer peptide
; NAME/KEY: PEPTIDE
; LOCATION: (17)..(37)
; OTHER INFORMATION: Amino acid sequence 947-967 of the Tetanus toxoid precursor (Te

OTHER INFORMATION: oxylysin
NAME/KEY: PEPTIDE
LOCATION: (38)..(41)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (42)..(50)
OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-18

Query Match 99.3%; Score 272; DB 9; Length 50;
Best Local Similarity 100.0%; Pred. No. 2.9e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGFSLNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 49
DB 2 HWSYGLRPGSSGFSLNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 49

RESULT 2

US-09-848-834A-14
Sequence 14, Application US/09848834A
Patent No. US20020076416A1
GENERAL INFORMATION:

APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A
CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 50/202,328
PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 14
LENGTH: 37

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the
OTHER INFORMATION: nRH hormone linked by a spacer to amino acid sequence 947-967 of
OTHER INFORMATION: the Tetanus toxoid precursor (Tentoxylisin)

NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline

NAME/KEY: PEPTIDE
LOCATION: (11)..(16)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone

NAME/KEY: PEPTIDE
LOCATION: (11)..(16)
OTHER INFORMATION: Spacer peptide

NAME/KEY: PEPTIDE
LOCATION: (17)..(37)
OTHER INFORMATION: (Tentoxylisin)

US-09-848-834A-14

Query Match 72.6%; Score 199; DB 9; Length 37;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 36; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 HWSYGLRPGSSGFSLNNFTVSFWLRVPKVSASHLE 37
DB 2 HWSYGLRPGSSGFSLNNFTVSFWLRVPKVSASHLE 37

RESULT 3

US-09-848-834A-10
Sequence 10, Application US/09848834A
Patent No. US20020076416A1
GENERAL INFORMATION:

APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 10
LENGTH: 34
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 947-967 of the
OTHER INFORMATION: Tetanus toxoid precursor (Tentoxylisin) linked by a spacer to an
OTHER INFORMATION: amino acid sequence 2-10 of the GnRH hormone
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Amidated phenylalanine
NAME/KEY: PEPTIDE
LOCATION: (1)..(21)
OTHER INFORMATION: Amino acids 947-967 of the Tetanus Toxoid Precursor
NAME/KEY: PEPTIDE
LOCATION: (22)..(25)
OTHER INFORMATION: Spacer peptide
NAME/KEY: PEPTIDE
LOCATION: (26)..(34)
OTHER INFORMATION: Amino acids 2-10 of the human GnRH hormone
NAME/KEY: MOD_RES
LOCATION: (34)..(34)
OTHER INFORMATION: Amidated glycine or glycineamide
US-09-848-834A-10

Query Match 67.5%; Score 185; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 9.5e-16;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 49
DB 1 FNNFTVSFWLRVPKVSASHLEGPSLHWSYGLRP 33

RESULT 4

US-09-848-834A-19
Sequence 19, Application US/09848834A
Patent No. US20020076416A1
GENERAL INFORMATION:

APPLICANT: Aphton Corporation
TITLE OF INVENTION: Chimeric Peptide Immunogens
FILE REFERENCE: 1102865-0047
CURRENT APPLICATION NUMBER: US/09/848,834A

CURRENT FILING DATE: 2001-05-04
PRIOR APPLICATION NUMBER: 60/202,328
PRIOR FILING DATE: 2000-05-05

NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
SEQ ID NO 19
LENGTH: 46
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of human
OTHER INFORMATION: GnRH linked by a spacer to amino acid sequence 830-844 of Tetan
OTHER INFORMATION: toxoid precursor (Tentoxylisin) linked by a spacer to amino aci
OTHER INFORMATION: sequence 1-10 of GnRH
NAME/KEY: MOD_RES
LOCATION: (1)..(1)
OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
NAME/KEY: MOD_RES
LOCATION: (46)..(46)
OTHER INFORMATION: Amidated glycine or glycineamide
NAME/KEY: PEPTIDE
LOCATION: (1)..(10)
OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
NAME/KEY: PEPTIDE

/ LOCATION: (11)..(16)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (17)..(31)
/ OTHER INFORMATION: Amino acid sequence 830-844 of the Tetanus toxin precursor
/ NAME/KEY: PEPTIDE (Tentoxylisin)
/ LOCATION: (32)..(37)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (38)..(46)
/ OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-19

Query Match 52.9%; Score 145; DB 9; Length 46;
Best Local Similarity 60.4%; Pred. No. 1.1e-10; Indels 4; Gaps 1;
Matches 29; Conservative 6; Mismatches 9;
Qy 2 HWSYGLRPGSGPSLNNFTVSWLRVPKVSASHLHSGPSLHWSYGLRP 49
Db 2 HWSYGLRPGSGPSLQYIKANSKFIGITELSS---GPSLHWSYGLRP 45

RESULT 5
US-09-848-834A-17
/ Sequence 17, Application US/09848834A
/ Patent No. US20020076416A1
/ GENERAL INFORMATION:
/ APPLICANT: Aptech Corporation
/ TITLE OF INVENTION: Chimeric Peptide Immunogens
/ CURRENT APPLICATION NUMBER: US/09/848,834A
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR FILING DATE: 2002-02-328
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 17
/ LENGTH: 47
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of the Gn
/ OTHER INFORMATION: RH hormone linked by a spacer to amino acid sequence 288-302 of
/ OTHER INFORMATION: the Measles virus protein F linked by a spacer to amino acid seq
/ OTHER INFORMATION: uence 2-10 of the GnRH hormone
/ NAME/KEY: MOD RES
/ LOCATION: (11)..(11)
/ OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
/ NAME/KEY: MOD RES
/ LOCATION: (47)..(47)
/ OTHER INFORMATION: Amidated-glycine or glycylamide
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(10)
/ OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
/ NAME/KEY: PEPTIDE
/ LOCATION: (11)..(18)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (19)..(34)
/ OTHER INFORMATION: Amino acid sequence 288-302 of the Measles virus fusion protein,
/ NAME/KEY: PEPTIDE
/ LOCATION: (35)..(38)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (39)..(47)
/ OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-17

Query Match 51.6%; Score 141.5; DB 9; Length 47;
Best Local Similarity 59.8%; Pred. No. 3e-10;
Matches 30; Conservative 1; Mismatches 11; Indels 9; Gaps 2;

Qy 2 HWSYGLRPGSGPSLNNFTVSWLRVPKVSASHL---EGPSLHWSYGLRP 49
Db 2 HWSYGLRPGSGPSL-----KLLSEIKGVIVHRLEGVEGPSLHWSYGLRP 46

RESULT 6

US-09-848-834A-20
/ Sequence 20, Application US/09848834A
/ Patent No. US20020076416A1
/ GENERAL INFORMATION:
/ APPLICANT: Aptech Corporation
/ TITLE OF INVENTION: Chimeric Peptide Immunogens
/ FILE REFERENCE: 1102865-0047
/ CURRENT APPLICATION NUMBER: US/09/848,834A
/ PRIOR FILING DATE: 2001-05-04
/ PRIOR FILING DATE: 2002-02-328
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20
/ LENGTH: 51
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Chimeric peptide consisting of amino acid sequence 1-10 of huma
/ OTHER INFORMATION: ium falciparum circumsporozoite (CSP) protein
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: Pyroglutamic acid or 5-oxoproline
/ NAME/KEY: MOD RES
/ LOCATION: (51)..(51)
/ OTHER INFORMATION: Amidated glycine or glycylamide
/ NAME/KEY: PEPTIDE
/ LOCATION: (1)..(10)
/ OTHER INFORMATION: Amino acid sequence 1-10 of the human GnRH hormone
/ NAME/KEY: PEPTIDE
/ LOCATION: (11)..(16)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (17)..(36)
/ OTHER INFORMATION: Amino acid sequence 378-398 of the Plasmodium falciparum
/ OTHER INFORMATION: circumsporozoite (CSP) protein
/ NAME/KEY: PEPTIDE
/ LOCATION: (37)..(42)
/ OTHER INFORMATION: Spacer peptide
/ NAME/KEY: PEPTIDE
/ LOCATION: (43)..(51)
/ OTHER INFORMATION: Amino acid sequence 2-10 of the human GnRH hormone
US-09-848-834A-20

Query Match 50.5%; Score 138.5; DB 9; Length 51;
Best Local Similarity 54.7%; Pred. No. 7.8e-10;
Matches 29; Conservative 4; Mismatches 11; Indels 9; Gaps 2;
Qy 2 HWSYGLRPGSGPSLNNFTVSWLRVPKVSASHLHSGPSLHWSYGLRP 49
Db 2 HWSYGLRPGSGPSLDEKXIA---KMEKASSVFNVNSSGSPSLHWSYGLRP 50

RESULT 7
US-10-295-074-46
/ Sequence 46, Application US/10295074
/ Publication No. US20030185845A1
/ GENERAL INFORMATION:
/ APPLICANT: Pharmexa A/S
/ TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
/ FILE REFERENCE: P1013DK00
/ CURRENT APPLICATION NUMBER: US/10/295,074
/ CURRENT FILING DATE: 2002-11-15
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 46

LENGTH: 194
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: hTNF with inserted tetanus toxoid P2 and P30 epitopes
NAME/KEY: MUTAGEN
LOCATION: (110)..(124)
OTHER INFORMATION: Tetanus toxoid P2 epitope (SEQ ID NO: 2)
FEATURE:
NAME/KEY: MUTAGEN
LOCATION: (125)..(145)
OTHER INFORMATION: Tetanus toxoid P30 epitope (SEQ ID NO: 3)
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (2)..(109)
OTHER INFORMATION: hTNF amino acids 1-108
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (146)..(194)
OTHER INFORMATION: hTNF amino acids 109-157
US-10-295-074-46

Query Match 44.9%; Score 123; DB 14; Length 194;
Best Local Similarity 82.1%; Pred. No. 2.7e-07;
Matches 23; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 16 LFNFTVSFWLRVPKVSASHLEGPSLHW 43
DB 124 LFNFTVSFWLRVPKVSASHLEAKPW 151

RESULT 8
US-10-295-074-13
Sequence 13, Application US/10295074
Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295, 074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.1
SEQ ID NO 13
LENGTH: 287
TYPE: PRT
FEATURE:
ORGANISM: Artificial sequence
OTHER INFORMATION: Two human IL5 monomers joined by diglycine linker and including
OTHER INFORMATION: terminally positioned P30 and P2 epitopes
US-10-295-074-13

Query Match 44.2%; Score 121; DB 14; Length 287;
Best Local Similarity 85.2%; Pred. No. 7.5e-07;
Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 14 PSLFNFTVSFWLRVPKVSASHLEGPS 40
DB 21 PTFNFTVSFWLRVPKVSASHLEIPT 47

RESULT 9
US-10-295-074-11
Sequence 11, Application US/10295074
Publication No. US20030185845A1
GENERAL INFORMATION:
APPLICANT: Pharmexa A/S
TITLE OF INVENTION: NOVEL IMMUNOGENIC MIMETICS OF MULTIMER PROTEINS
FILE REFERENCE: P1013DK00
CURRENT APPLICATION NUMBER: US/10/295, 074
CURRENT FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 285
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: 2 human IL5 monomers joined by P2 and P30 epitopes
US-10-295-074-11

Query Match 43.8%; Score 120; DB 14; Length 285;
Best Local Similarity 92.0%; Pred. No. 9.8e-07;
Matches 23; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 16 LFNFTVSFWLRVPKVSASHLEGPS 40
DB 149 LFNFTVSFWLRVPKVSASHLEIPT 173

RESULT 10
US-10-297-942-18
Sequence 18, Application US/10297942
Publication No. US20030185816A1
GENERAL INFORMATION:
APPLICANT: Ferring BV
TITLE OF INVENTION: Solubilised Protein Vaccines
FILE REFERENCE: P68445USO
CURRENT APPLICATION NUMBER: US/10/297, 942
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: PCT/DK01/00431
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: DK PA 2000 00966
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 18
LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
US-10-297-942-18

Query Match 43.2%; Score 118.5; DB 14; Length 158;
Best Local Similarity 80.6%; Pred. No. 7.8e-07;
Matches 25; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 7 LRPSSGSPSLFNFTVSFWLRVPKVSASHLE 37
DB 2 VRSSRTPS-FNNFTVSFWLRVPKVSASHLE 31

RESULT 11
US-10-297-942-12
Sequence 12, Application US/10297942
Publication No. US20030185816A1
GENERAL INFORMATION:
APPLICANT: Ferring BV
TITLE OF INVENTION: Solubilised Protein Vaccines
FILE REFERENCE: P68445USO
CURRENT APPLICATION NUMBER: US/10/297, 942
CURRENT FILING DATE: 2003-04-21
PRIOR APPLICATION NUMBER: PCT/DK01/00431
PRIOR FILING DATE: 2001-10-16
PRIOR APPLICATION NUMBER: DK PA 2000 00966
PRIOR FILING DATE: 2000-06-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 12
LENGTH: 158
TYPE: PRT
ORGANISM: Homo sapiens
US-10-297-942-12

Query Match 43.1%; Score 118; DB 14; Length 158;
Best Local Similarity 100.0%; Pred. No. 9e-07;